

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 12.81 Seconds
(without alignments)
35.679 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	77	A01259	complement C3 - pi
2	30	100.0	111	I48204	colipase - nutria
3	30	100.0	351	MFN2B3	matrix protein - p
4	30	100.0	401	T46306	hypothetical prote
5	30	100.0	530	G64918	phosphotransferase
6	30	100.0	530	F85768	PTS system, maltos
7	30	100.0	584	S06696	hypothetical prote
8	30	100.0	1009	D75399	probable penicilli
9	28	93.3	230	H83001	probable permease
10	28	93.3	285	T12342	major intrinsic pr
11	28	93.3	494	S16068	testosterone 15alp
12	28	93.3	494	B33531	cytochrome p450 2A
13	28	93.3	494	B47494	cytochrome p450 2A
14	28	93.3	494	A32030	coumarin 7-monoxy
15	28	93.3	494	A33531	testosterone 15alp
16	28	93.3	527	F83368	probable aldehyde
17	27	90.0	132	T29072	hypothetical prote
18	27	90.0	175	G72683	hypothetical prote
19	27	90.0	179	S65534	light-harvesting c
20	27	90.0	190	T29068	hypothetical prote
21	27	90.0	202	C84305	hypothetical prote
22	27	90.0	213	S75247	hypothetical prote
23	27	90.0	256	F96510	light-harvesting c
24	27	90.0	256	T52328	chlorophyll a/b-bi
25	27	90.0	280	T04049	chlorophyll a/b-bi
26	27	90.0	286	S16294	chlorophyll a/b-bi
27	27	90.0	302	S31865	chlorophyll a/b-bi
28	27	90.0	376	E70680	probable prob - My
29	27	90.0	379	C81809	hypothetical prote

ALIGNMENTS

RESULT 1

A01259

complement C3 - pig (fragment)

N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit
C:Species: Sus scrofa domestica (domestic pig)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: A01259

R:Corbin, N.C.; Hugli, T.E.

J. Immunol. 117, 990-995, 1976

A:Title: The primary structure of porcine C3a anaphylatoxin.

A:Reference number: A01259; MUID:76263261

A:Accession: A01259

A:Molecule type: protein

A:Residues: 1-77 <COR>

A:Note: three disulfide bonds are present
C:Comment: Complement C3 contains two chains, formed by removal of four residues and
alternative complement pathways, releases the C3a anaphylatoxin from the amino end o
native-complement-pathway C3/C5 convertase.

C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.

C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by
C:Comment: The major site of synthesis of this plasma protein is the liver.

C:Superfamily: alpha-2-macroglobulin

C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprote

F:1-77/Product: complement C3a anaphylatoxin #status experimental <C3a>

Query Match 100.0%; Score 30; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 72 PLGLAR 77

RESULT 2

I48204

colipase - nutria

C:Species: Myocastor coypus (nutria, coypu)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C:Accession: I48204

R:Thirstrup, K.; Carriere, F.; Hjorth, S.A.; Rasmussen, P.B.; Nielsen, P.F.; Ladefog
Eur. J. Biochem. 227, 186-193, 1995

A:Title: Cloning and expression in insect cells of two pancreatic lipases and a proco

A:Reference number: I48204; MUID:95154288

A:Accession: I48204

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-111 <RES>

A:Cross-references: EMBL:X82998; MID:g599866; PIDN:CAA58119.1; PTD:g599867

C:Superfamily: colipase

probable cation-tr
heat shock protein
leukemia virus cel
al-mating type pro
probable 3-demethy
hypothetical prote
CbrA protein - Erw
NADH dehydrogenase
probable periplasm
hypothetical prote
fructose-6-P phosph
pyrophosphate--fru
hypothetical prote
fructose-6-P phosph
oxalyl-CoA decarbo
penicillin-binding

```

Query Match          100.0%; Score 30; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 50 PLGLAR 55

RESULT 3
MFNBZ3
matrix protein - parainfluenza virus type 3
C:Species: parainfluenza virus type 3
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: D27502
R:Sakai, Y.; Suzu, S.; Shioda, T.; Shibuta, H.
Nucleic Acids Res. 15, 2927-2944, 1987
A:Title: Nucleotide sequence of the bovine parainfluenza 3 virus genome: its 3' end and
A:Reference number: A93658; MUID:87174818
A:Accession: D27502
A:Molecule type: genomic RNA
A:Residues: 1-351 <SAK>
A:Cross-references: EMBL:X00114; NID:g60891; PIDN:CAA68296.1; PID:g60895
C:Genetics:
A:Gene: M
C:Superfamily: parainfluenza virus matrix protein
C:Keywords: matrix protein

Query Match          100.0%; Score 30; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 93 PLGLAR 98

RESULT 4
T46306
hypothetical protein DKFZp434D2411.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46306
R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223035
A:Accession: T46306
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-401 <AAA>
A:Cross-references: EMBL:AL137599
A:Experimental source: adult testis; clone DKFZp434D2411
C:Genetics:
A:Note: DKFZp434D2411.1

Query Match          100.0%; Score 30; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 126 PLGLAR 131

RESULT 5
G64918
phosphotransferase system enzyme II (EC 2.7.1.69) factor II, maltose- and glucose-specific
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: G64918; B42477; PV0011
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64918
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-530 <BLAT>
A:Cross-references: GB:AE000258; GB:U00096; NID:g2367121; PIDN:AACT4693.1; PID:g17879
A:Experimental source: strain K-12, substrain MG1655
R:Reidl, J.; Boos, W.
J. Bacteriol. 173, 4862-4876, 1991
A:Title: The malX maly operon of Escherichia coli encodes a novel enzyme II of the ph
alose system.
A:Reference number: A42477; MUID:91310596
A:Accession: B42477
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143, 'Y', 145-295, 'N', 297-431, 'R', 433-530 <REI>
A:Cross-references: GB:M60722; NID:g146690; PIDN:AAA24098.1; PID:g146692
R:Reidl, J.; Roemisch, K.; Ehrmann, M.; Boos, W.
J. Bacteriol. 171, 4888-4899, 1989
A:Title: MalX, a novel protein involved in regulation of the maltose system of Escher
A:Reference number: JVO031; MUID:89359124
A:Accession: PV0011
A:Molecule type: DNA
A:Residues: 1-119, AFQOPRPLKRRRTKNAKAFHDKMRKLTFRASNETDVLITAFYSLHGDPRF' <RE2>
A:Cross-references: GB:M28539; NID:g146707; PIDN:AAA24103.1; PID:g146708
C:Genetics:
A:Gene: malX
A:Map position: 36 min
C:Function:
A:Description: mediates transport of glucose and maltose across the cytoplasmic membr
r concentration
C:Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phosph
C:Keywords: phosphoprotein; phosphotransferase; sugar transport system; transmembrane
F:7-528/Domain: phosphotransferase system glucose-specific enzyme II, factor II homol
F:22-38/Domain: transmembrane #status predicted <TM01>
F:73-89/Domain: transmembrane #status predicted <TM02>
F:99-115/Domain: transmembrane #status predicted <TM03>
F:146-162/Domain: transmembrane #status predicted <TM04>
F:185-201/Domain: transmembrane #status predicted <TM05>
F:321-337/Domain: transmembrane #status predicted <TM06>
F:354-370/Domain: transmembrane #status predicted <TM07>
F:399-415/Domain: transmembrane #status predicted <TM08>
F:493-510/Domain: transmembrane #status predicted <TM09>
F:471/Active site: Cys (phosphocysteine intermediate) #status predicted

Query Match          100.0%; Score 30; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 86 PLGLAR 91

RESULT 6
F85768
PTS system, maltose and glucose-specific II ABC [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85768
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A95480; MUID:21074935; PMID:11206551
A:Accession: F85768
A>Status: preliminary

```

Nucleoside diphosphate kinase (EC 2.7.4.6) cytochrome P450 2A5 isoform 2
testosterone 15alpha-hydroxylase (EC 1.1.1.61) testosterone 15alpha-hydroxylase
C:Species: Mus musculus (house mouse)
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 04-Mar-2000
C:Accession: S16068
R:Squires, E.J.; Negishi, M.
J. Biol. Chem. 263, 4166-4171, 1988

A;Title: Reciprocal regulation of sex-dependent expression of testosterone 15-alpha-hydroxysteroid oxidoreductase (EC 1.1.1.61)
A;Reference number: S16067; MUID:88153731
A;Accession: S16068
A;Molecule type: mRNA
A;Residues: 1-494 <SQ>
A;Cross-references: EMBL:M19319
C;Genetics:
A;Gene: CYP2A3
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metalloprotein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 12
B33531
cytochrome P450 2A3.2 - mouse
N;Contains: oxidoreductase (EC 1.1.1.61)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Mar-2000
C;Accession: B33531; B30499
R;Lindberg, R.; Burkhardt, B.; Ichikawa, T.; Negishi, M.
J. Biol. Chem. 264, 6465-6471, 1989
A;Title: The structure and characterization of type I P-450-15-alpha gene as major steroid hydroxylase
A;Reference number: A33531; MUID:89197954
A;Accession: B33531
A;Molecule type: DNA
A;Residues: 1-494 <LIN>
A;Cross-references: GB:M25211; GB:J04631; NID:g193826; PIDN:AAA37798.1; PID:g387191
A;Accession: B30499
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-494 <li2>
A;Cross-references: GB:M25211; GB:J04631; NID:g193826; PIDN:AAA37798.1; PID:g387191
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 13
B47494
cytochrome P450 2A11 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 04-Mar-2000
C;Accession: B47494; JC2553
R;Peng, H.M.; Ding, X.; Coon, M.J.
J. Biol. Chem. 268, 17253-17260, 1993
A;Title: Isolation and heterologous expression of cloned cDNAs for two rabbit nasal mucin glycoproteinase
A;Reference number: A47494; MUID:93352510
A;Accession: B47494
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-494 <PEN>
A;Cross-references: GB:L10237; NID:g165434; PIDN:AAA31372.1; PID:g165435

R;Ding, X.; Peng, H.M.; Coon, M.J.
Biochem. Biophys. Res. Commun. 203, 373-378, 1994
A;Title: Structure-function analysis of CYP2A10 and CYP2A11, P450 cytochromes that di
A;Reference number: JC2552; MUID:94354829
A;Contents: annotation
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; transmembrane protein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 14
A32030
cumarin 7-monooxygenase (EC 1.14.14.-) cytochrome P450 2A3 - rat
N;Alternate names: coumarin 7-hydroxylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 28-Jul-2000
C;Accession: S15056; S12708; A32030
R;Ueno, T.; Gonzalez, F.
submitted to the EMBL Data Library, March 1990
A;Description: Complete sequence of the rat CYP2A3 gene specifically transcribed in l
A;Reference number: S15056
A;Accession: S15056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-494 <UEN>
A;Cross-references: EMBL:M33190; NID:g203750; PIDN:AAA41022.1; PID:g203751
R;Ueno, T.; Gonzalez, F.J.
Nucleic Acids Res. 18, 4623-4624, 1990
A;Title: Complete sequence of the rat CYP2A3 gene specifically transcribed in lung.
A;Reference number: S12708; MUID:90356430
A;Accession: S12708
A;Molecule type: DNA
A;Residues: 1-108, 'G', 110-334, 'N', 336-494 <UE2>
A;Cross-references: EMBL:M33190
A;Note: the authors translated the codon AAG for residue 326 as Leu, TTT for residue
R;Kimura, S.; Kozak, C.A.; Gonzalez, F.J.
Biochemistry 28, 3798-3803, 1989
A;Title: Identification of a novel P450 expressed in rat lung: cDNA cloning and sequ
A;Reference number: A32030; MUID:89323084
A;Accession: A32030
A;Molecule type: mRNA
A;Residues: 8-108, 'G', 110-334, 'N', 336-494 <KIM>
A;Cross-references: GB:J02852; NID:g703260; PIDN:AAA88511.1; PID:g703261
C;Genetics:
A;Gene: CYP2A3
A;Introns: 60/3; 115/1; 165/1; 218/3; 277/3; 325/1; 387/3; 435/1
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; meta
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 15
A33531

testosterone 15alpha-monooxygenase (EC 1.14.14.-) cytochrome P450 2a4 - mouse
N:Alternate names: cytochrome P450(15-alpha) I
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence.Revision 31-Mar-1992 #text_change 03-Nov-2000
C:Accession: A33531; A30499; S16067; I55275; I70052
R:Lindberg, R.; Burkhardt, B.; Ichikawa, T.; Negishi, M.
J. Biol. Chem. 264, 6463-6471, 1989
A:Title: The structure and characterization of type I P-450-15-alpha gene as major steroid
A:Reference number: A33531; MUID:89197954
A:Accession: A33531
A:Molecule type: DNA
A:Residues: 1-494 <LIN1>
A:Cross-references: GB:M26208; GB:J04631; NID:gl93816; PIDN:AAA37797.1; PID:g387190
A:Accession: A30499
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-494 <LIN2>
A:Cross-references: GB:M26208; GB:J04631; NID:gl93816; PIDN:AAA37797.1; PID:g387190
R:Squires, E.J.; Negishi, M.
J. Biol. Chem. 263, 4166-4171, 1988
A:Title: Reciprocal regulation of sex-dependent expression of testosterone 15-alpha-hydroxylase
A:Reference number: S16067; MUID:88153731
A:Accession: S16067
A:Molecule type: mRNA
A:Residues: 1-295, 'Q', 297-305, 'G', 307-494 <SQU>
A:Cross-references: EMBL:J03549; NID:g201970; PIDN:AAA40426.1; PID:g201971; GB:M19319; N
C:Genetics:
A:Gene: Cyp2a4
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F:298-461/Domain: cytochrome P450 homology <p45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg1ar 6
|:|:|:|
Db 367 FMGLAR 372

Search completed: February 28, 2002, 16:47:23
Job time: 78 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:25 ; Search time 10.14 Seconds
(without alignments)
21.695 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	77	1	P01025 sus scrofa
2	30	100.0	111	1	P42889 myocastor c
3	30	100.0	351	1	P06166 bovine para
4	30	100.0	530	1	P19642 escherichia
5	30	100.0	584	1	P15255 zymomonas m
6	30	100.0	867	1	P98167 bos taurus
7	28	93.3	142	1	O32347 caulobacter
8	28	93.3	421	1	P54991 streptomyce
9	28	93.3	494	1	P20812 rattus norv
10	28	93.3	494	1	P15392 mus musculu
11	28	93.3	494	1	P20852 mus musculu
12	28	93.3	494	1	O05556 oryctolagus
13	27	90.0	376	1	P71910 mycobacteri
14	27	90.0	631	1	Q9rbn6 streptomyce
15	27	90.0	679	1	P33125 ajellomyces
16	27	90.0	843	1	Q03368 bos taurus
17	26	86.7	233	1	P79374 trichosurus
18	26	86.7	305	1	Q47084 erwinia chr
19	26	86.7	394	1	P93306 arabidopsis
20	26	86.7	439	1	P20190 streptomyce
21	26	86.7	526	1	P27353 methylosinu
22	26	86.7	554	1	Y514 SYN3
23	26	86.7	568	1	OXC_OXAFO
24	26	86.7	853	1	PBPA_HAEIN
25	26	86.7	1050	1	ULK1_HUMAN
26	25	83.3	114	1	CH60_MYCUL
27	25	83.3	116	1	CB2D_LYCES
28	25	83.3	120	1	CH60_MYCAG
29	25	83.3	120	1	CH60_MYCAS
30	25	83.3	120	1	CH60_MYCCI
31	25	83.3	120	1	CH60_MYCFA
32	25	83.3	120	1	CH60_MYCGN
33	25	83.3	120	1	CH60_MYCGO

34	25	83.3	120	1	CH60_MYCGS
35	25	83.3	120	1	CH60_MYCIT
36	25	83.3	120	1	CH60_MYCKA
37	25	83.3	120	1	CH60_MYCNO
38	25	83.3	120	1	CH60_MYCPH
39	25	83.3	120	1	CH60_MYCPV
40	25	83.3	120	1	CH60_MYCRH
41	25	83.3	120	1	CH60_MYCVA
42	25	83.3	127	1	CB21_EUGGR
43	25	83.3	143	1	YBIF_SALTY
44	25	83.3	150	1	CB22_PINSY
45	25	83.3	151	1	CH60_MYCAV

ALIGNMENTS

RESULT 1

ID	CO3A_PIG	STANDARD;	PRT;	77 AA.
AC	P01025;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	COMPLEMENT C3A ANAPHYLATOXIN.			
GN	C3.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=76263261; PubMed=956663;			
RA	Corbin N.C., Hugli T.E.;			
RT	"The primary structure of porcine C3a anaphylatoxin.";			
RL	J. Immunol. 117:990-995(1976).			
CC	-1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,			
CC	C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT			
CC	INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR			
CC	PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND			
CC	BASOPHILIC LEUKOCYTES.			
CC	-1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.			
DR	PIR; A01259; C3PGAT.			
DR	HSSP; P01031; 1KJS.			
DR	InterPro; IPR001599; Alpha_2_macroglubln.			
DR	InterPro; IPR000020; Anaphylatoxin.			
DR	InterPro; IPR001840; Anaphylatoxn.			
DR	Pfam; PF01821; ANATO; 1.			
DR	PRINTS; PR00004; ANAPHYLATOXN.			
DR	SMART; SM00104; ANATO; 1.			
DR	PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.			
DR	PROSITE; PS01177; ANAPHYLATOXIN_1; 1.			
DR	PROSITE; PS01178; ANAPHYLATOXIN_2; 1.			
KW	Complement pathway; Complement alternate pathway; Plasma;			
KW	Inflammatory response.			
FT	DOMAIN 22 57 ANAPHYLATOXIN-LIKE.			
FT	DISULFID 22 49 BY SIMILARITY.			
FT	DISULFID 23 56 BY SIMILARITY.			
FT	DISULFID 36 57 BY SIMILARITY.			
SQ	SEQUENCE 77 AA; 9085 MW; 7ECB22E619533429 CRC64;			

Query Match 100.0%; Score 30; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 72 PLGLAR 77

RESULT 2
COL_MYOCO

Q49373	mycobacteri
Q49564	mycobacteri
Q49594	mycobacteri
Q50255	mycobacteri
Q50270	mycobacteri
Q50271	mycobacteri
Q50373	mycobacteri
Q50827	mycobacteri
P12327	euglena gra
P74867	salmonella
P15192	pinus sylve
Q48900	mycobacteri

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ID COL_MYOCO STANDARD; PRT; 111 AA.
AC P42889;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE COLIPASE PRECURSOR.
GN CLPS.

OS Myocastor copys (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-41.
RC TISSUE=Pancreas;
RX MEDLINE=95154288; PubMed=7851384;
RA Thirstup K., Carrier F., Hjorth S.A., Rasmussen P.B., Nielsen P.F.,
RA Ladefoged C., Thim L., Boel E.;
RT "Cloning and expression in insect cells of two pancreatic lipases and
RT a procolipase from Myocastor copys.";
RL Eur. J. Biochem. 227:186-193(1995).
CC -!- FUNCTION: COLIPASE IS A COFACTOR OF PANCREATIC LIPASE. IT ALLOWS
CC THE LIPASE TO ANCHOR ITSELF TO THE LIPID-WATER INTERFACE. WITHOUT
CC COLIPASE THE ENZYME IS WASHED OFF BY BILE SALTS, WHICH HAVE AN
CC INHIBITORY EFFECT ON THE LIPASE.
CC -!- FUNCTION: ENTEROSTATIN HAS A BIOLOGICAL ACTIVITY AS A SATIETY
CC SIGNAL (BY SIMILARITY).
CC -!- SUBUNIT: FORM A 1:1 STOICHIOMETRIC COMPLEX WITH PANCREATIC LIPASE.
CC -----
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CC -----
CC EMBL; X62998; CAA58119.1; -.
CC HSSP; P02703; IPCO.
CC InterPro; IPR001981; Colipase.
CC Pfam; PF01114; Colipase; 1.
CC PRINTS; PR00128; COLIPASE.
CC SMART; SM00023; COLIPASE; 1.
CC PROSITE; PS00121; COLIPASE; 1.
KW Lipid degradation; Digestion; Pancreas; Signal.
FT SIGNAL 1 17
FT PROPEP 18 22 ENTEROSTATIN, ACTIVATION PEPTIDE
FT FT CHAIN 23 111
FT FT COLIPASE.
FT FT DISULFID 34 45 BY SIMILARITY.
FT FT DISULFID 40 56 BY SIMILARITY.
FT FT DISULFID 44 78 BY SIMILARITY.
FT FT DISULFID 66 86 BY SIMILARITY.
FT FT DISULFID 80 104 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11899 MW; 7FF37DE7C169616B CRC64;

Query Match 100.0%; Score 30; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
DB 50 PLGLAR 55

RESULT 3
VMAAT_PT3B STANDARD; PRT; 351 AA.
AC P06166;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

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DE GN MATRIX PROTEIN.
OS Bovine parainfluenza 3 virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX NCBI_TaxID=11215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=910N;
RX MEDLINE=87174818; PubMed=3031614;
RA Sakai Y., Suzu S., Shioda T., Shibuta H.;
RT "Nucleotide sequence of the bovine parainfluenza 3 virus genome: its
RT 3' end and the genes of NP, P, C and M proteins.";
RL Nucleic Acids Res. 15:2927-2944(1987).
CC -!- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY
CC AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL
CC MEMBRANE.
CC -----
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CC -----
CC EMBL; Y00114; CAA68296.1; -.
CC EMBL; D84095; BAA12216.1; -.
CC PIR; D27502; MFNZB3
CC InterPro; IPR000982; Matrix.
CC Pfam; PF00661; Matrix; 1.
CC ProDom; PD000741; Matrix; 1.
KW Matrix protein; Envelope protein.
SQ SEQUENCE 351 AA; 39310 MW; C7749FC19EA79535 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
DB 93 PLGLAR 98

RESULT 4
PTOA_ECOLI STANDARD; PRT; 530 AA.
AC P19642; P77621;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PTS SYSTEM. MALTOSE AND GLUCOSE-SPECIFIC IIABC COMPONENT (MALTOSE AND
DE GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
DE COMPONENT) (EC 2.7.1.69).
GN MALX OR B1621.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91310596; PubMed=1856179;
RA Reidl J., Boos W.;
RT "The malX maly operon of Escherichia coli encodes a novel enzyme II
RT of the phosphotransferase system recognizing glucose and maltose and
RT an enzyme abolishing the endogenous induction of the maltose
RT system.";
RL J. Bacteriol. 173:4862-4876(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

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RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RC MEDLINE=97251357; PubMed=9097039;
 RX Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Samei G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [4]
 RN PRELIMINARY SEQUENCE OF 1-177 FROM N.A.
 RX MEDLINE=89359124; PubMed=2670898;
 RA Reidel J., Romisch K., Ehrmann M., Boos W.;
 RT "MalI, a novel protein involved in regulation of the maltose system
 of *Escherichia coli*, is highly homologous to the repressor proteins
 GalR, CytR, and LacI.";
 RL J. Bacteriol. 171:4888-4899(1989).
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
 CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
 CC -TRANSPORT SYSTEM. THE IID DOMAINS CONTAIN THE SUGAR BINDING SITE
 CC AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
 CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
 CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
 CC THE SUGAR.
 CC -1- FUNCTION: MALX ENCODES A PHOSPHOTRANSFERASE SYSTEM ENZYME II THAT
 CC CAN RECOGNIZE GLUCOSE AND MALTOSE AS SUBSTRATES EVEN THOUGH THESE
 CC SUGARS MAY NOT REPRESENT THE NATURAL SUBSTRATES OF THE SYSTEM.
 CC -1- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
 CC PROTEIN HISTIDINE + SUGAR PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
 CC -1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
 CC -1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
 CC -----
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 CC -----
 CC EMBL; M60722; AAA24098.1; -;
 CC EMBL; AE000258; AAC74693.1; -;
 CC EMBL; D90805; BAA15372.1; -;
 CC EMBL; D90806; BAA15379.1; -;
 CC EMBL; D90808; BAA15409.1; -;
 CC EMBL; M28539; AAA24103.2; ALT_SEQ.
 CC PIR; PV0011; PV0011.
 CC PIR; B42477; B42477.
 CC HSP; P05053; IIBA.
 CC EcoGene; EG10563; malX.
 CC InterPro; IPR001996; PTS_EIIB.
 CC InterPro; IPR003352; PTS_EIIC.
 CC Pfam; PF00367; PTS_EIIB; 1.
 CC Pfam; PF02378; PTS_EIIC; 1.
 CC ProDom; PD001476; PTS_EIIB; 1.
 CC ProSITE; PS01035; PTS_EIIB_CYS; 1.
 KW Phosphotransferase system; Sugar transport; Transferase;
 KW Transmembrane; Inner membrane; Phosphorylation; Complete proteome.
 FT DOMAIN 1 ? EIIA DOMAIN

FT DOMAIN 452 ? ?
 FT MOD_RES 240 486 EIIC DOMAIN.
 FT MOD_RES 356 240 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 471 356 PHOSPHORYLATION (BY SIMILARITY).
 FT TRANSMEM 22 42 POTENTIAL.
 FT TRANSMEM 47 67 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 289 309 POTENTIAL.
 FT TRANSMEM 321 341 POTENTIAL.
 FT TRANSMEM 343 363 POTENTIAL.
 FT TRANSMEM 369 389 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT CONFLICT 144 144 I -> Y (IN REF. 1).
 FT CONFLICT 296 296 P -> N (IN REF. 1).
 FT CONFLICT 432 432 E -> R (IN REF. 1).
 SQ SEQUENCE 530 AA; 56627 MW; 042E9817955975BF CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 530;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 plglar 6
 Db 86 PLGLAR 91
 RESULT 5
 65KD_ZYMMO STANDARD; PRT; 584 AA.
 ID 65KD_ZYMMO
 AC P15255;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 65 KDA PROTEIN (ORF 1).
 OS Zymomonas mobilis.
 OG Plasmid pZM2.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 OX NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10988 / ZM1;
 RA Misawa N., Nakamura K.;
 RT "The nucleotide sequence of the 2.7 kilobase pair plasmid of *Zymomonas*
 RT mobilis ATCC 10988.";
 RL J. Biotechnol. 12:63-70(1989).
 CC -----
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 CC -----
 CC EMBL; X14438; CAA32611.1; -;
 CC PIR; S06696; S06696.
 CC InterPro; IPR001668; Mob_Pre.
 CC InterPro; IPR002936; Toprim.
 CC Pfam; PF01076; Mob_Pre; 1.
 CC Pfam; PF01751; Toprim; 1.
 CC SMART; SM00493; TOPRIM; 1.
 KW Plasmid.
 SQ SEQUENCE 584 AA; 65793 MW; 0402D2FB569B65A6 CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 584;

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Best Local Similarity 100.0%; Pred. NO. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
DB 170 PLGLAR 175

RESULT 6
SSPO_BOVIN STANDARD; PRT; 867 AA.
AC P98167;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SCO-SPONDIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ependymocyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinel R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastugue B., Meinel A.;
RT "SCO-spondin: a new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation." ;
RL J. Cell Sci. 109:1053-1061(1996).
CC -!- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC -!- DEVELOPMENTAL STAGE: EMBRYO.
CC -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
CC -!- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
CC -----
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CC -----
DR EMBL; X93922; CAA63815.1; -
DR HSSP; P01130; 1AJJ.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR002919; TIL.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWFC.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; ldl_recept_a; 3.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00090; tsp_1; 4.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00192; LDLA; 3.
DR SMART; SM00209; TSP1; 4.
DR SMART; SM00214; VWC; 1.
DR SMART; SM00011; VWC_def; 1.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 1.
DR PROSITE; PS01209; LDLRA_1; 3.
DR PROSITE; PS00668; LDLRA_2; 3.
DR PROSITE; PS50068; LDLRA_2; 3.
DR PROSITE; PS50092; TSP1; 4.
DR GlycoProtex; G1_1
KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
FT NON_TER

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FT DOMAIN 26 81 TSP TYPE-1 1.
FT DOMAIN 103 142 EGF-LIKE 1.
FT DOMAIN 143 180 EGF-LIKE 2.
FT DOMAIN 185 243 TSP TYPE-1 2.
FT DOMAIN 344 502 F5/8 TYPE C.
FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 762 813 TSP TYPE-1 3.
FT DOMAIN 814 867 TSP TYPE-1 4.
FT DISULFID 107 122 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT DISULFID 149 169 BY SIMILARITY.
FT DISULFID 171 179 BY SIMILARITY.
FT DISULFID 344 502 BY SIMILARITY.
FT DISULFID 508 520 BY SIMILARITY.
FT DISULFID 515 533 BY SIMILARITY.
FT DISULFID 527 542 BY SIMILARITY.
FT DISULFID 665 677 BY SIMILARITY.
FT DISULFID 672 690 BY SIMILARITY.
FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 867;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
DB 347 PLGLAR 352

RESULT 7
DKSA_CAUCR STANDARD; PRT; 142 AA.
ID DKSA_CAUCR AC 032347;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNAK SUPPRESSOR PROTEIN HOMOLOG.
DN DKSA OR CC2580.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB15N / NA1000;
RX MEDLINE=98215187; PubMed=9555902;
RA Mohr C.D., Mackichan J.K., Shapiro L.;
RT "A membrane-associated protein, Flx, is required for an early step in
RT Caulobacter flagellar assembly." ;
RL J. Bacteriol. 180:2175-2185(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

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RA Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RP SEQUENCE OF 1-76 FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA Ely B.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 DKSA/TRAR-TYPE ZINC FINGER.
CC -!- SIMILARITY: IN THE N-TERMINAL HALF, TO THE N-TERMINAL OF
CC B. SUBTILIS YTEA.
CC -----
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CC -----
CC EMBL; AF034413; AAC38353.1;
DR EMBL; AE005926; AAK24550.1;
DR EMBL; M91448; AAB83954.1;
DR TIGR; CC2580;
DR InterPro; IPR000962; Znf_dskA_trar.
DR Pfam; PF01258; zf_dskA_trar; 1.
DR PRINTS; PRO0618; DKSZNFINGER.
DR PROSITE; PS01102; DKSA_TRAR_ZN_FINGER; FALSE_NEG.
KW Zinc-finger; Complete proteome.
FT ZN_FING 104 128 TRAR/DKSA-TYPE.
FT CONFLICT 137 137 R -> P (IN REF. 1).
SQ SEQUENCE 142 AA; 16774 MW; 8824F2DD9827B89C CRC64;
Query Match 93.38; Score 28; DB 1; Length 142;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 plglar 6
Db 110 PIGLAR 115
RESULT 8
ID SNAA_STRPR STANDARD; PRT; 421 AA.
AC P54991;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE PRISTINAMYCIN IIA SYNTHASE SUBUNIT A (PIIA SYNTHASE SUBUNIT A).
GN SNAA.
OS Streptomyces pristinaespiralis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=38300;
RN SEQUENCE FROM N.A.
RC STRAIN=SP92;
RX MEDLINE=95394837; PubMed=7665509;
RA Blanc V., Lagneau D., Didier P., Gil P., Lacroix P., Crouzet J.;
RT "Cloning and analysis of structural genes from Streptomyces
RT pristinaespiralis encoding enzymes involved in the conversion of
RT pristinamycin IIB to pristinamycin IIA (PIIA): PIIA synthase and
RT NADH:riboflavin 5'-phosphate oxidoreductase.";
RL J. Bacteriol. 177:5206-5214(1995).
RN [2]
RP SEQUENCE OF 1-18 AND 364-383.
RX MEDLINE=95394836; PubMed=7665508;
RA Thibaut D., Ratet N., Bisch D., Faucher D., Debussche L., Blanche F.;
RT "Purification of the two-enzyme system catalyzing the oxidation of
RT the D-proline residue of pristinamycin IIB during the last step of
RT pristinamycin IIA biosynthesis.";

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RL J. Bacteriol. 177:5199-5205(1995).
CC -!- FUNCTION: CATALYZES THE OXIDATION OF THE PROLINE RESIDUE OF
CC PRISTINAMYCIN IIB (PIIB) TO PRISTINAMYCIN IIA (PIIA).
CC -!- COFACTOR: FMN.
CC -!- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SNAA AND SNAB.
CC -!- SIMILARITY: BELONGS TO THE NTAA/SNAA/SOXA(DSZA) FAMILY OF
CC MONOOXYGENASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U21215; AAA83563.1;
DR Oxidoreductase; Monooxygenase; Flavoprotein; FMN.
FT INIT_MET 0
SQ SEQUENCE 421 AA; 46373 MW; 341AD008A939CEFA CRC64;
Query Match 93.38; Score 28; DB 1; Length 421;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 plglar 6
Db 187 PIGIAR 192
RESULT 9
ID CPA3_RAT STANDARD; PRT; 494 AA.
AC P20812;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 2A3 (EC 1.14.14.1) (CYPIIA3) (COUMARIN 7-HYDROXYLASE).
GN CYP2A3 OR CYP2A-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
RX MEDLINE=90356430; PubMed=2388852;
RA Ueno T., Gonzalez F.;
RT "Complete sequence of the rat CYP2A3 gene specifically transcribed in
RT lung.";
RL Nucleic Acids Res. 18:4623-4624(1990).
RN [2]
RP SEQUENCE OF 8-494 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=89323084; PubMed=2751996;
RA Kimura S., Kozak C.A., Gonzalez F.J.;
RT "Identification of a novel P450 expressed in rat lung: cDNA cloning
RT and sequence, chromosome mapping, and induction by
RT 3-methylcholanthrene.";
RL Biochemistry 28:3798-3803(1989).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: LUNG.
CC -!- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----

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01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME P450 2A5 (EC 1.14.14.1) (CYPIIA5) (COUMARIN 7-HYDROXYLASE)
(P450-15-COH) (P450-ITA3.2).
CYP2A5 OR CYP2A-5).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=89197954; PubMed=2703500;
RA Lindberg R., Burkhardt B., Ichikawa T., Negishi M.;
RT "The structure and characterization of type I P-450(15) alpha gene as
RT major steroid 15 alpha-hydroxylase and its comparison with type II P-
RT 450(15) alpha gene";
RL J. Biol. Chem. 264:6465-6471(1989).
[2]
SEQUENCE FROM N.A.
RP STRAIN=17NC/Z;
RC Jounaidi Y.;
RA "cDNA and amino acid sequence of a new cyp2a isoform overexpressed in
RT chemically induced mouse hepatoma";
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[3]
MUTAGENESIS.
RP MEDLINE=89281737; PubMed=2733794;
RA Lindberg R., Negishi M.;
RT "Alteration of mouse cytochrome P450c10 substrate specificity by
RT mutation of a single amino-acid residue.";
RL Nature 339:632-634(1989).
[4]
TISSUE SPECIFICITY.
RP MEDLINE=99421934; PubMed=10490589;
RA Lavery D.J., Lopez-Molina L., Margueron R., Fleury-Olela F.,
RC Conquet F., Schibler U., Bonfils C.;
RT "Circadian expression of the steroid 15 alpha-hydroxylase (Cyp2a4) and
RT coumarin 7-hydroxylase (Cyp2a5) genes in mouse liver is regulated by
RT the PAR leucine zipper transcription factor DBP";
RL Mol. Cell. Biol. 19:6488-6499(1999).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: LIVER, WITH A STRONG CIRCADIAN RHYTHMICITY.
CC CIRCADIAN EXPRESSION IS REGULATED BY DBP.
CC -!- DEVELOPMENTAL STAGE: IN LIVER; ACTIVITY 6 FOLD HIGHER IN FEMALES
CC THAN IN MALES.
CC -!- MISCELLANEOUS: THERE ARE ONLY 11 DIFFERENCES BETWEEN THE SEQUENCE
CC OF TESTOSTERONE 15-ALPHA-HYDROXYLASE AND THAT OF COUMARIN 7-
CC HYDROXYLASE. BY SITE-DIRECTED MUTAGENESIS IT HAS BEEN SHOWN THAT
CC MODIFICATION OF POSITION 209 IS SUFFICIENT TO CONVERT THE
CC SPECIFICITY OF THE TWO FORMS OF THE ENZYME.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; M25211; AAA37798.1; -
EMBL; M26204; AAA37798.1; JOINED.
EMBL; M25205; AAA37798.1; JOINED.
EMBL; M25206; AAA37798.1; JOINED.
EMBL; M25207; AAA37798.1; JOINED.
EMBL; M25208; AAA37798.1; JOINED.
EMBL; M25209; AAA37798.1; JOINED.
EMBL; M25210; AAA37798.1; JOINED.
EMBL; X89864; CAA61963.1; -

PIR; B33531; B33531.
MGD; MGI:88597; Cyp2a5.
InterPro: IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00463; EP450I.
PROSITE; PS00086; CYTOCHROME_P450; 1.
OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 439 439 HEME.
SQ SEQUENCE 494 AA; 56740 MW; 1C2516D5FA2551D0 CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgilar 6
Db 367 PMGLAR 372

RESULT 12
CPAB_RABIT
ID CPAB_RABIT STANDARD; PRT; 494 AA.
AC Q05556;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 2A11 (EC 1.14.14.1) (CYP1IA11) (P450-IIA11).
GN CYP2A11.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=NEW ZEALAND WHITE; TISSUE=Nasal mucosa;
RC MEDLINE=93352510; PubMed=8349611;
RA Peng H.M., Ding X., Coon M.J.;
RT "Isolation and heterologous expression of cloned cDNAs for two rabbit
RT nasal microsomal proteins, CYP2A10 and CYP2A11, that are related to
RT nasal microsomal cytochrome P450 form a.";
RL J. Biol. Chem. 268:17253-17260(1993).
CC -!- FUNCTION: CATALYZES THE OXYGENATION OF A VARIETY OF SUBSTRATES,
CC INCLUDING ETHANOL AND PROCARINOLIGENS SUCH AS N-NITROSODIETHYLAMINE
CC AND PHENACETIN. HAS NO OR LITTLE ACTIVITY AS A COUMARIN 7-
CC HYDROXYLASE.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER AND LUNG AS WELL AS IN
CC NASAL TISSUES.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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EMBL; L10237; AAA31372.1; -
InterPro: IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00463; EP450I.
PROSITE; PS00086; CYTOCHROME_P450; 1.
OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 439 439 HEME (BY SIMILARITY).
SQ SEQUENCE 494 AA; 57277 MW; 28D2E5C4E5D0861A CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
 Db 367 PWGLAR 372

RESULT 13
 PROB_MYCTU STANDARD; PRT; 376 AA.
 AC P71910;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GLUTAMATE 5-KINASE (EC 2.7.2.11) (CAMMA-GLUTAMYL KINASE) (GK).
 GN PROB OR RV2439C OR MT2515 OR MTCY428.07.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE -> ADP + L-GLUTAMATE
 CC 5-PHOSPHATE (PRODUCT RAPIDLY CYCLIZES TO 5-OXOPROLINE AND
 CC ORTHOPHOSPHATE).
 CC -!- PATHWAY: FIRST STEP IN PROLINE BIOSYNTHESIS PATHWAY.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z81451; CAB03780.1; -;
 CC EMBL: AE007089; AAK46812.1; -;
 CC TIGR: MT2515; -;
 CC TubercuList; RV2439c; -;
 CC InterPro; IPR001048; AakKinase.
 CC InterPro; IPR001057; Glut_5_kinase.
 CC InterPro; IPR002478; PUA.
 CC Pfam; PF00696; aakKinase; 1.

DR Pfam; PF01472; PUA; 1.
 DR PRINTS: PR00474; GLUSKINASE.
 DR SMART: SM00359; PUA; 1.
 DR PROSITE: PS00902; GLUTAMATE_5_KINASE; 1.
 KW Transferase; Kinase; Proline biosynthesis; Complete proteome.
 FT CONFLICT 226 226 A -> S (IN REF. 2).
 SQ SEQUENCE 376 AA; 38788 MW; AC7BB65C0B302E6A CRC64;

Query Match 90.0%; Score 27; DB 1; Length 376;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
 Db 67 PLGLSR 72

RESULT 14
 DXS_STRC1 STANDARD; PRT; 631 AA.
 ID DXS_STRC1
 AC Q9REN6;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE (EC 2.2.-.-) (1-DEOXYXYLULOSE-
 DE 5-PHOSPHATE SYNTHASE) (DXP SYNTHASE) (DXPS).
 GN DXS.
 OS Streptomyces sp. (strain CL190).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=93372;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20115529; PubMed=10648511;
 RA Kuzuyama T., Takagi M., Takahashi S., Seto H.;
 RT "Cloning and characterization of 1-deoxy-D-xylulose 5-phosphate
 RT synthase from Streptomyces sp. Strain CL190, which uses both the
 RT mevalonate and nonmevalonate pathways for isopentenyl diphosphate
 RT biosynthesis.";
 RL J. Bacteriol. 182:891-897(2000).
 CC -!- FUNCTION: CATALYZES THE ACYLOIN CONDENSATION REACTION BETWEEN C
 CC ATOMS 2 AND 3 OF PYRUVATE AND GLYCERALDEHYDE 3-PHOSPHATE TO YIELD
 CC 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXP).
 CC -!- COFACTOR: THIAMINE PYROPHOSPHATE. REQUIRES MANGANESE OR MAGNESIUM.
 CC -!- PATHWAY: DEOXYXYLULOSE-5-PHOSPHATE PATHWAY (DXP) OF ISOPRENOID
 CC BIOSYNTHESIS: FIRST STEP. BIOSYNTHETIC PATHWAY TO THIAMINE AND
 CC PYRIDOXOL; FIRST STEP.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- MISCELLANEOUS: OPTIMAL TEMPERATURE IS 42-44 DEGREES CELSIUS AND
 CC OPTIMAL PH IS 9.0.
 CC -!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY. DXS SUBFAMILY.
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 CC -----
 CC EMBL: AB026631; BAA5847.1; -;
 CC InterPro; IPR000360; Transketolase.
 CC PROSITE; PS00801; TRANSKETOLASE_1; 1.
 CC PROSITE; PS00802; TRANSKETOLASE_2; FALSE_NEG.
 KW Transferase; Flavoprotein; Thiamine biosynthesis; Manganese; Magnesium.
 KW Isoprene biosynthesis; Thiamine biosynthesis; Manganese; Magnesium.
 SQ SEQUENCE 631 AA; 67961 MW; 306042CDFA287694 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 631;
 Best Local Similarity 83.3%; Pred. No. 14e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 28, 2002, 16:50:30
Job time: 185 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:05 ; Search time 22.98 Seconds
(without alignments)
38.191 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	103	2 P72389	P72389 streptomyce
2	30	100.0	193	6 O97940	O97940 sus scrofa
3	30	100.0	351	12 Q9J7D9	Q9J7D9 bovine para
4	30	100.0	351	12 Q9J7D3	Q9J7D3 bovine para
5	30	100.0	401	4 Q9NT09	Q9NT09 homo sapien
6	30	100.0	430	4 Q9ULP6	Q9ULP6 homo sapien
7	30	100.0	469	4 Q9NVE1	Q9NVE1 homo sapien
8	30	100.0	484	4 Q9NVU9	Q9NVU9 homo sapien
9	30	100.0	489	11 Q9D1E5	Q9D1E5 mus musculus
10	30	100.0	523	2 P96159	P96159 vibrio furn
11	30	100.0	549	2 Q9RL52	Q9RL52 streptomyce
12	30	100.0	1009	2 Q9RUG9	Q9RUG9 deinococcus
13	30	100.0	1661	6 Q9GKPI	Q9GKPI sus scrofa
14	28	93.3	104	11 Q9D1S5	Q9D1S5 mus musculus
15	28	93.3	230	2 Q9HU29	Q9HU29 pseudomonas
16	28	93.3	285	10 Q40259	Q40259 mesembryant
17	28	93.3	491	2 Q9A7T1	Q9A7T1 caulobacter
18	28	93.3	494	11 Q9QZ50	Q9QZ50 mesocricetu
19	28	93.3	527	2 Q911Q0	Q911Q0 pseudomonas

20	28	93.3	708	4	Q9UGU9	Q9UGU9 homo sapien
21	28	93.3	861	12	O90599	O90599 human immun
22	28	93.3	941	3	O9C2P5	O9C2P5 neurospora
23	28	93.3	1353	4	O9Y6Y1	O9Y6Y1 homo sapien
24	27	90.0	65	4	Q9UH04	Q9UH04 homo sapien
25	27	90.0	100	11	Q9CUD1	Q9CUD1 mus musculu
26	27	90.0	114	12	Q9DW90	Q9DW90 rat cytomeg
27	27	90.0	132	2	O86523	O86523 streptomyce
28	27	90.0	175	1	Q9YDM6	Q9YDM6 aeropyrum p
29	27	90.0	185	10	Q38688	Q38688 amphidinium
30	27	90.0	190	2	O86520	O86520 streptomyce
31	27	90.0	192	12	O55942	O55942 human immun
32	27	90.0	202	1	Q9HPR0	Q9HPR0 halobacteri
33	27	90.0	213	2	P73135	P73135 synechocyst
34	27	90.0	227	10	Q9FEM1	Q9FEM1 galdieria s
35	27	90.0	256	10	Q9XF85	Q9XF85 arabidopsis
36	27	90.0	286	10	Q9CF39	Q9CF39 arabidopsis
37	27	90.0	280	10	Q9XF89	Q9XF89 arabidopsis
38	27	90.0	286	10	Q00321	Q00321 lycopersico
39	27	90.0	302	10	Q41040	Q41040 pinus sylve
40	27	90.0	360	2	Q9A2D1	Q9A2D1 caulobacter
41	27	90.0	379	2	Q9JRB5	Q9JRB5 neisseria m
42	27	90.0	429	10	Q9LIT6	Q9LIT6 oryza sativ
43	27	90.0	443	4	Q9UEW4	Q9UEW4 homo sapien
44	27	90.0	479	10	Q9M903	Q9M903 arabidopsis
45	27	90.0	660	2	O69710	O69710 mycobacteri

ALIGNMENTS

RESULT 1
ID P72389 PRELIMINARY; PRT; 103 AA.
AC P72389;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HISTIDINE KINASE HOMOLOG (ABS1) AND RESPONSE REGULATOR HOMOLOG
DE (ABS2) GENES, COMPLETE CDS (FRAGMENT).
D7.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J1501;
RX MEDLINE=96236039; PubMed=8655502;
RA Brian P., Riggie P.J., Santos R.A., Champness W.C.;
RT "Global negative regulation of Streptomyces coelicolor antibiotic
RT synthesis mediated by an absA-encoded putative signal transduction
RT system".
RL J. Bacteriol. 178:3221-3231(1996).
DR EMBL; U51332; AAB08051.1; -
DR InterPro; IPR001687; ATP_GTP_A.
FT NON_TER 103
SQ SEQUENCE 103 AA; 10989 MW; BA0C3C8424268398 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 94 PLGLAR 99

RESULT 2
O97940
ID O97940 PRELIMINARY; PRT; 193 AA.
AC O97940;

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-JUN-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COMPLEMENT COMPONENT 3 (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RA Miner J.L., Toombs C.F.;
RT "Porcine acylation stimulating protein.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110278; AAC9785.1; -.
DR HSP; P01031; 1KJS.
DR InterPro: IPR001599; Alpha_2_macroglobln.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxn.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01821; ANATO; 1.
DR PRINTS; SM00104; ANAPHYLATOXN.
DR SMART; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
FT NON_TER 1
FT CHAIN 64 >139 PUTATIVE ACYLATION STIMULATING PROTEIN.
FT NON_TER 193 193
FT SEQUENCE 193 AA; 22117 MW; 08787595DE3E1713 CRC64;

Query Match 100.0%; Score 30; DB 6; Length 193;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 135 PLGLAR 140

RESULT 3
Q9J7D9
ID Q9J7D9 PRELIMINARY; PRT; 351 AA.
AC Q9J7D9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MATRIX M.
OS Bovine parainfluenza 3 virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX NCBI_TaxID=11215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KANSAS/15626/84;
RA Bailey J.E., McAuliffe J.M., Skiadopoulos M.H., Collins P.L.,
RA Murphy B.R.;
RT "Sequence determination and molecular analysis of two strains of
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL bovine parainfluenza virus type 3 that are attenuated for primates.";
DR EMBL; AF178654; AAF28256.1; -.
DR InterPro: IPR000982; Matrix.
DR Pfam; PF00661; Matrix; 1.
DR ProDom; PD000741; Matrix; 1.
DR SEQUENCE 351 AA; 39300 MW; 8C0C389DA2C925B2 CRC64;

Query Match 100.0%; Score 30; DB 12; Length 351;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 135 PLGLAR 140

Query Match 100.0%; Score 30; DB 6; Length 193;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 135 PLGLAR 140

Query Match 100.0%; Score 30; DB 12; Length 351;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 135 PLGLAR 140

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Db 93 PLGLAR 98

RESULT 4
Q9J7D3
ID Q9J7D3 PRELIMINARY; PRT; 351 AA.
AC Q9J7D3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MATRIX M.
OS Bovine parainfluenza 3 virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX NCBI_TaxID=11215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIPPING FEVER;
RA Bailey J.E., McAuliffe J.M., Skiadopoulos M.H., Collins P.L.,
RA Murphy B.R.;
RT "Sequence determination and molecular analysis of two strains of
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL bovine parainfluenza virus type 3 that are attenuated for primates.";
DR EMBL; AF178655; AAF28262.1; -.
DR InterPro: IPR000982; Matrix.
DR Pfam; PF00661; Matrix; 1.
DR ProDom; PD000741; Matrix; 1.
DR SEQUENCE 351 AA; 39327 MW; 9739B537D0DBCC27 CRC64;

Query Match 100.0%; Score 30; DB 12; Length 351;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 93 PLGLAR 98

RESULT 5
Q9NT09
ID Q9NT09 PRELIMINARY; PRT; 401 AA.
AC Q9NT09;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 45.2 KDA PROTEIN (FRAGMENT).
GN DKFZP34D241.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137599; CAB70835.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 401 AA; 45220 MW; A1A6D50C5D204AC3 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 126 PLGLAR 131

RESULT 6

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Q9ULP6          PRELIMINARY;          PRT;      430 AA.
ID Q9ULP6;
AC Q9ULP6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE KIAA1174 PROTEIN (FRAGMENT).
GN KIAA1174.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB033000; BAA86488.1; -.
FT NON_TER
SQ SEQUENCE 430 AA; 48A05 MW; 684C67BD3F60DFD CRC64;

Query Match          100.0%; Score 30; DB 4; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 251 PLGLAR 256

RESULT 7
Q9NVE1          PRELIMINARY;          PRT;      469 AA.
ID Q9NVE1;
AC Q9NVE1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CDNA FLJ10789 FIS, CLONE NT2RP4000500.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001651; BAA91811.1; -.
SQ SEQUENCE 469 AA; 53215 MW; 181059F23AD87DF5 CRC64;

Query Match          100.0%; Score 30; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 214 PLGLAR 219

RESULT 8
Q9NVU9          PRELIMINARY;          PRT;      484 AA.
ID Q9NVU9;
AC Q9NVU9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CDNA FLJ10494 FIS, CLONE NT2RP2000283.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Tanahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001356; BAA91646.1; -.
SQ SEQUENCE 484 AA; 53901 MW; C309EED810F4796A CRC64;

Query Match          100.0%; Score 30; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 209 PLGLAR 214

RESULT 9
Q9D1E5          PRELIMINARY;          PRT;      489 AA.
ID Q9D1E5;
AC Q9D1E5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1110013E13RIK PROTEIN.
GN 1110013E13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003656; BAB22919.1; -.
DR MGD; MGI:1922025; 1110013E13RIK.
SQ SEQUENCE 489 AA; 54957 MW; 50AA85EF2C58B79A CRC64;

Query Match          100.0%; Score 30; DB 11; Length 489;

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Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 plglar 6
DB 214 PLGLAR 219

RESULT 10
P6159          PRELIMINARY; PRT; 523 AA.
ID P96159;
AC P96159;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PTS PERMEASE FOR GLUCOSE.
GN MALX.
OS Vibrio furnissii.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=29494;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SR1514;
RX MEDLINE=97125987; PubMed=8969209;
RA Bouma C.L., Roseman S.;
RT "Sugar transport by the marine chitinolytic bacterium Vibrio
RT furnissii. Molecular cloning and analysis of the glucose and N-
RT acetylglucosamine permeases.";
RL J. Biol. Chem. 271:33457-33467(1996).
DR EMBL; U65013; AAC44676.1; -.
DR HSSP; P05053; IIBA.
DR InterPro; IPR001996; PTS_EIIB.
DR InterPro; IPR003352; PTS_EIIC.
DR Pfam; PF00367; PTS_EIIB; 1.
DR Pfam; PF02378; PTS_EIIC; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
SQ SEQUENCE 523 AA; 55932 MW; 90D03CD004A3FE48 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 84 PLGLAR 89

RESULT 11
Q9RL52          PRELIMINARY; PRT; 549 AA.
ID Q9RL52;
AC Q9RL52;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SUGAR PHOSPHOTRANSFERASE.
GN MALX.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Murphy L., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

STRAIN-A3(2);
MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kisser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL121596; CAB56664.1; -.
DR HSSP; P05053; IIBA.
DR InterPro; IPR001996; PTS_EIIB.
DR InterPro; IPR003352; PTS_EIIC.
DR Pfam; PF00367; PTS_EIIB; 1.
DR Pfam; PF02378; PTS_EIIC; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
SQ SEQUENCE 549 AA; 58601 MW; F4750674A78D850A CRC64;

Query Match 100.0%; Score 30; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 83 PLGLAR 88

RESULT 12
Q9RUG9          PRELIMINARY; PRT; 1009 AA.
ID Q9RUG9;
AC Q9RUG9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PENICILLIN-BINDING PROTEIN 1B MCRB, PUTATIVE.
GN DR1417.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001986; AAF10981.1; -.
DR TIGR; DR1417; -.
DR InterPro; IPR001264; Transglycosyl.
DR InterPro; IPR001460; Transpeptidse.
DR Pfam; PF00912; Transglycosyl; 1.
DR Pfam; PF00905; Transpeptidase; 1.
DR ProDom; PD001895; Transglycosyl; 1.
KW Complete proteome.
SQ SEQUENCE 1009 AA; 111165 MW; 4B9A9508C5E52B72 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 1009;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 121 PLGLAR 126
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RESULT 13
Q9GKPI PRELIMINARY; PRT; 1661 AA.
AC Q9GKPI; 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COMPLEMENT COMPONENT C3.
GN C3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Wimmers K., Ponsuksilli S., Schmolli F., Schellander K.;
RT "Molecular genetic analysis of the porcine C3 gene.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154933; AAG40565.1; -;
DR InterPro; IPR002890; A2M.N.
DR InterPro; IPR001599; Alpha_2_macroglobulin.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M.N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
SQ SEQUENCE 1661 AA; 186806 MW; 4899D0914BE3310C CRC64;

Query Match 100.0%; Score 30; DB 6; Length 1661;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 741 PLGLAR 746

RESULT 14
Q9DLS5 PRELIMINARY; PRT; 104 AA.
AC Q9DLS5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1100001D15RIK PROTEIN.
GN 1100001D15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003155; BAB22609.1; -;
DR MGD; MGI:1915679; l100001D15RIK.
SQ SEQUENCE 104 AA; 11682 MW; 14EFBF0AEB02A3CC CRC64;

Query Match 93.3%; Score 28; DB 11; Length 104;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 20 PLGLAR 25

RESULT 15
Q9HU29 PRELIMINARY; PRT; 230 AA.
AC Q9HU29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PROBABLE PERMEASE OF ABC TRANSPORTER.
GN PA5155.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goitry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; AE004928; AAG08540.1; -;
DR InterPro; IPR000515; BPD_transp. 1.
DR Pfam; PF00528; BPD_transp. 1.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBR; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 230 AA; 26155 MW; FC9F0CF5DA374316 CRC64;

Query Match 93.3%; Score 28; DB 2; Length 230;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 38 PLGLAR 43

Search completed: February 28, 2002, 16:50:13
Job time: 188 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 23.88 Seconds
(without alignments)
18.611 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	6	18	3-methylcholanthrene
2	30	100.0	6	19	Matrix metallopro
3	30	100.0	8	5	Sequence of peptid
4	30	100.0	77	22	Pig C3a anaphylato
5	30	100.0	103	20	N-terminal fragmen
6	30	100.0	351	11	Viral membrane pro
7	30	100.0	362	22	Human secreted pro
8	30	100.0	459	22	Human polypeptide
9	30	100.0	469	22	Human protein sequ
10	30	100.0	484	22	Human protein sequ
11	30	100.0	489	21	Amino acid sequenc

12	30	100.0	489	21	AAV66660	Membrane-bound pro
13	30	100.0	489	22	AA38703	Human polypeptide
14	30	100.0	489	22	AA65183	Human PRO783 (UNQ4
15	30	100.0	538	22	AA40489	Human polypeptide
16	30	100.0	538	22	AA40490	Human polypeptide
17	30	100.0	1061	20	AAW87504	Human N-methyl-D-a
18	30	100.0	1081	21	AA826240	Human N-methyl-D-a
19	30	100.0	1212	20	AAW87503	Human N-methyl-D-a
20	30	100.0	1232	21	AA826239	Human N-methyl-D-a
21	28	93.3	422	15	AA54202	snak gene product
22	27	90.0	134	22	AAU04893	Micromonospora eve
23	27	90.0	159	21	AA826215	Arabidopsis thalia
24	27	90.0	159	21	AA826215	Arabidopsis thalia
25	27	90.0	161	21	AA826187	Arabidopsis thalia
26	27	90.0	217	22	AA893531	Human protein sequ
27	27	90.0	224	20	AA74086	Human prostate tum
28	27	90.0	230	22	AA895751	Human protein sequ
29	27	90.0	256	21	AA828186	Arabidopsis thalia
30	27	90.0	265	21	AA828185	Arabidopsis thalia
31	27	90.0	272	21	AA826214	Arabidopsis thalia
32	27	90.0	272	21	AA826214	Arabidopsis thalia
33	27	90.0	275	19	AA48847	Rat receptor tyros
34	27	90.0	280	21	AA826213	Arabidopsis thalia
35	27	90.0	280	21	AA826213	Arabidopsis thalia
36	27	90.0	376	22	AA811188	Mycobacterium tube
37	27	90.0	404	21	AA858135	Arabidopsis thalia
38	27	90.0	417	21	AA858134	Arabidopsis thalia
39	27	90.0	419	21	AA858133	Arabidopsis thalia
40	27	90.0	450	22	AA891347	C glutamicum prote
41	27	90.0	472	19	AAW48848	Human receptor tyr
42	27	90.0	604	18	AAW42400	Partial sequence o
43	27	90.0	745	22	AA867331	Human neuron proge
44	26	86.7	46	22	AA863399	Human breast cance
45	26	86.7	48	21	AAV65041	Human 5' EST relat

ALIGNMENTS

RESULT 1
AAB74602
ID AAB74602 standard; peptide; 6 AA.

AC AAB74602;
DT 21-MAY-2001 (first entry)
XX
DE 3-methylcholanthrene (MCA) peptide substrate.
XX

XX 3-methylcholanthrene; MCA; substrate; metalloproteinase inhibitor;
KW cancer; metastasis; arthritis.
XX

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "pro in N-terminally modified to
FT 7-methoxycoumarin-4-yl-acetyl-pro"

FT Modified-site 5 /note= "Ala is N-terminally modified to
FT 3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl-ala"

FT Modified-site 6 /note= "amidated"

XX WO9720824-A1.

XX 12-JUN-1997..

XX 05-DEC-1996; 96WO-US19328.

XX 08-DEC-1995; 95US-0569766.

XX (AGOU-) AGOURON PHARM INC.

XX Zook SE, Dagnino R, Deason ME, Bender SL, Melnick MJ;
 XX 'WPI'; 1997-332465/30.
 XX
 PT New N-hydroxy-benzenesulphonyl carboxamide derivatives - are
 PT metallo-protease inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 XX Example 22; Page 108; 151pp; English.
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. N-hydroxy benzenesulphonyl (thiazine or piperazine)
 CC carboxamide derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 2
 AAWS2139
 ID AAWS2139 standard; Peptide; 6 AA.
 XX
 AC AAWS2139;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Matrix metalloproteinase MMP-9 substrate B.
 XX
 KW Membrane-type matrix metalloproteinase; MT1-MMP;
 KW matrix metalloproteinase 12; MMP-12; osteoclastic proteinase;
 KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;
 KW bone resorption; metastasis; tumour; cancer; ulcer; arthritis;
 KW periodontal disease; therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Mca-proline"
 FT Cleavage-site 3..4
 FT Modified-site 5
 FT /note= "Dpa-alanine"
 XX
 XX WO9804287-A1.
 XX
 XX 05-FEB-1998.
 XX
 XX 29-JUL-1997; 97WO-EP04110.
 XX
 XX 30-JUL-1996; 96GB-0015976.
 XX
 XX (CLIN-) CENT CLINICAL & BASIC RES.
 PA
 PI Delaïsse J, Foged NT, Meldal M;
 XX
 XX WPI; 1998-130425/12.
 XX
 PT Use of inhibitors of protease(s) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as
 PT osteoporosis
 XX
 PS Example 6b; Page 44; 110pp; English.
 XX
 CC Peptide B is a substrate of matrix metalloproteinase MMP-9. Novel
 CC peptide substrate mimicking MMP-inhibitors (see AAWS2132-33) are
 CC promising agents for use in treatment of bone metabolic disease.
 CC They can be used to inhibit proteinases involved in the
 CC recruitment, proliferation, differentiation or migration of
 CC osteoclast precursor cells or in the migration, fusion, attachment,
 CC polarisation, removal of mineralised osseous substance or death of
 CC osteoclasts. The inhibitors reduce the rate of bone resorption
 CC and are used to treat or prevent, e.g. osteoporosis and osteolytic
 CC bone metastases. They are also useful in, e.g. treatment of
 CC cancer, ulcers, arthritis and periodontal disease.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 3
 AAP40579
 ID AAP40579 standard; peptide; 8 AA.
 XX
 AC AAP40579;
 XX
 DT 13-FEB-1992 (first entry)
 XX
 DE Sequence of peptides which control smooth muscle contraction,
 DE histamine release and vascular permeability.
 XX
 KW Asthma therapy; bronchial allergy; inflammatory response.
 XX
 PN US4438029-A.
 XX
 PD 20-MAR-1984.
 XX
 PF 21-FEB-1979; 79US-0013176.
 XX
 PR 21-FEB-1979; 79US-0013176.
 PR 25-JAN-1977; 77US-0762427.
 PR 19-JAN-1978; 78US-0870713.
 XX
 XX (RESE) RESEARCH CORP.
 XX
 XX Erickson BW, Hugli TE;
 XX
 XX WPI; 1984-088186/14.
 XX
 PT Peptides contg. Gly-Leu-Ala-Arg sequence - useful in promotion or
 PT inhibition of smooth muscle contraction, histamine release and
 PT vascular permeability
 XX
 PS Claim 6; column 7; 5pp; English.
 XX
 CC Gly-Leu-Ala-Arg (I) and peptides contg. (I) with Arg as the carboxyl
 CC terminus, contract smooth muscle, release histamine from mast cells
 CC and enhance vascular permeability. Peptides contg. the unit (I)-Gly
 CC are antagonists of this activity. The peptide with a carboxy
 CC terminus canavanine residue behaves similarly to those with Arg in
 CC this posn. Doses may be up to 2g or more per day, e.g. in units of
 CC 250mg.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 3 plglar 8

RESULT 4

AAE05446
 ID AAE05446 standard; Protein: 77 AA.

XX AC AAE05446;

DT 24-SEP-2001 (first entry)

DE DE Pig C3a anaphylatoxin.

XX Mannan binding protein-associated serine protease; MASP;
 KW complement-activation; C-activation; microbial infection;
 KW cyomegalovirus; CMV; hepatitis virus; human immunodeficiency virus;
 KW HIV; organ transplant rejection; tissue injury; autoimmune disease;
 KW rheumatoid arthritis; systemic lupus erythematosus; SLE;
 KW inflammatory response; Alzheimer's disease; pig; C3a anaphylatoxin.

XX OS Sus scrofa.

XX PN US6235494-B1.

XX PD 22-MAY-2001.

XX PF 08-FEB-1999; 99US-0246500.

XX PR 08-FEB-1999; 99US-0246500.

XX (SCRI) SCRIPPS RES INST.

XX PA Hugli TE;

XX WPI; 2001-450082/48.

XX Method for determining in-vivo levels of activated mannan binding
 PT protein-associated serine protease enzyme, and new peptide derivatives

XX Claim 3; Column 43-44; 39pp; English.

XX The invention relates to assays for measuring in-vivo levels of
 CC activated mannan-binding protein-associated serine protease (MASP-1 and
 CC MASP-2) activity. The assay comprises contacting a sample of blood or
 CC plasma comprising a metal ion chelator with a substrate of formula:
 CC R-peptide-Y; wherein the peptide comprises at least 4 residues from the
 CC C-terminus of an anaphylatoxin selected from C3a, C4a and C5a; R is a
 CC peptide blocking, protecting or capping group; and Y is any group
 CC cleavable from the substrate by MASP and comprises a labelled tag. The
 CC substrate of the invention is also useful for monitoring in vitro and
 CC in vivo complement-activation (C-activation) by classical, alternative
 CC or lectin pathways. The assays of MASP activity can be used for
 CC detecting or monitoring a condition associated with complement
 CC activation. The conditions include microbial infections
 CC caused by particularly cytomegalovirus (CMV), hepatitis virus and
 CC human immunodeficiency virus (HIV), organ transplant rejection, tissue
 CC injury, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE)) and inflammatory responses (e.g. in Alzheimer's
 CC disease and bacterial diseases). The assay of MASP is also useful for
 CC assessing the toxicity or injury of therapeutic treatments or screening
 CC test compounds as agents for treatment of viral diseases, parasitic
 CC infections, tissue injury, organ transplant rejection, autoimmune
 CC diseases or inflammatory responses. The present sequence is pig C3a
 CC anaphylatoxin.

XX SQ Sequence 77 AA;

Query Match 100.0%; Score 30; DB 22; Length 77;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 72 plglar 77

RESULT 5

AAW78493
 ID AAW78493 standard; Protein: 103 AA.

XX AC AAW78493;

XX 21-MAY-1999 (first entry)

DE DE N-terminal fragment S.coelicolor D7 protein.

XX AbsA; operon; open reading frame; histidine kinase; response regulator;
 KW mutation; insertion; antibiotic; actinorhodin; undecylprodigiosin.

XX OS Streptomyces coelicolor.

XX PN US5876987-A.

XX PD 02-MAR-1999.

XX PF 06-FEB-1997; 96US-0796414.

XX PR 07-FEB-1996; 96US-0011286.

XX PR 06-FEB-1997; 97US-0796414.

XX (UNMS) UNIV MICHIGAN STATE.

XX PI Anderson TB, Brian P, Champness WC;

XX WPI; 1999-189640/16.

XX N-PSDB; AAX21397.

XX Recombinant Streptomyces species - useful for the production of
 PT recombinant proteins and the hyper-expression of antibiotics,
 PT particularly actinorhodin and undecylprodigiosin

XX Disclosure; Fig 4; 30pp; English.

XX The sequences AAX21397-X21399 represent overlapping sequences from the
 CC AbsA operon of Streptomyces coelicolor. This sequence corresponds to
 CC the N-terminal portion of the D7 protein. The invention relates to
 CC the AbsA protein (AAW78491) which is a histidine kinase and the related
 CC protein AbsA2 (AAW78492) (also encoded by the operon) which is a
 CC response regulator for the AbsI gene. Inactivation of the AbsI gene
 CC either by mutation or insertion of heterologous DNA into the AbsI gene
 CC results in a Streptomyces organism which can hyperproduce heterologous
 CC proteins or antibiotics, especially actinorhodin and undecylprodigiosin.

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 30; DB 20; Length 103;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 94 plglar 99

RESULT 6

AAR06024
ID AAR06024 standard; protein; 351 AA.

XX AC AAR06024;

DT 04-DEC-1990 (first entry)

XX DE Viral membrane protein.

XX KW Haemagglutinin neuraminidase; vaccine; parainfluenza; ds.

XX OS Bovine parainfluenza type III virus.

XX PN JP02156883-A.

XX PD 15-JUN-1990.

XX PF 09-DEC-1988; 88JP-0311655.

XX PR 09-DEC-1988; 88JP-0311655.

XX PA (JAPG) NIPPON ZEON KK.

XX DR WPI; 1990-228484/30.

XX DE N-PSDB; AAQ05320.

XX PT Recombinant vaccinia virus - is which all or part of DNA coding
membrane fusion protein in combined to genom region.

XX PS Disclosure; ; p; Japanese.

XX CC Fragment of parainfluenza viral membrane fusion protein encoding DNA
may be incorporated into the vaccina virus, which may then be used
as a live vaccine for cows.

XX SQ Sequence 351 AA;

Query Match 100.0%; Score 30; DB 11; Length 351;
Best Local Similarity 100.0%; Pred. No. 45;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 piglar 6

Db 93 piglar 98

RESULT 7

AAG89160
ID AAG89160 standard; Protein; 362 AA.

XX AC AAG89160;

DT 11-SEP-2001 (first entry)

XX DE Human secreted protein, SEQ ID NO: 280.

XX KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
GENSET.

XX OS Homo sapiens.

XX PN WO200142451-A2.

XX PD 14-JUN-2001.

XX PF 07-DEC-2000; 2000WO-IB01938.

XX XX 08-DEC-1999; 99US-0169629.

XX PR 06-MAR-2000; 2000US-0187470.

XX XX (GENSET) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S;

XX WPI; 2001-367870/38.

XX DR N-PSDB; AAH64763.

XX PT Full length GENSET human nucleic acids encoding potentially secreted
proteins, useful in gene therapy and vaccination against a variety of
diseases, and for diagnosis of those diseases -

XX PS Claim 21; Page 816; 921pp; English.

XX CC The invention relates to full length GENSET human nucleic acids encoding
potentially secreted proteins. The nucleic acids and the polypeptides
they encode may be used in the prevention, treatment and diagnosis of
diseases associated with inappropriate GENSET gene expression. For
example, they be used to treat disorders associated with decreased
GENSET gene expression by rectifying mutations or deletions in a
patient's genome that affect the activity of GENSET or by supplementing
the patients own production of GENSET polypeptides. Conversely,
antisense nucleic acid molecules may be administered to down regulate
GENSET expression by binding with the cells' own genes and preventing
their expression. The sense and antisense nucleic acids may also be
used as DNA probes in diagnostic assays to detect and quantitate the
presence of similar nucleic acid sequences in samples, and hence to
determine which patients may be in need of restorative therapy.
The GENSET polypeptides may be used as antigens in the production of
antibodies and in assays to identify modulators (agonists and
antagonists) of GENSET polypeptide expression and activity. The
present sequence is a GENSET polypeptide of the invention.

XX SQ Sequence 362 AA;

Query Match 100.0%; Score 30; DB 22; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 piglar 6

Db 87 piglar 92

RESULT 8

AAM38704

ID AAM38704 standard; Protein; 469 AA.

XX AC AAM38704;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 1849.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US34263.

XX XX 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 XX WPI: 2001-442253/47.
 DR N-PSDB; AA157860.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Example 3: SEQ ID NO 1849; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA138642-AA142213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 469 AA;
 SQ

Query Match 100.0%; Score 30; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 |||||
 Db 214 plglar 219

RESULT 9
 AAB93173
 ID AAB93173 standard; Protein; 469 AA.
 AC
 XX AAB93173;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:12110.
 XX
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.

XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 XX WPI: 2001-318749/34.
 DR
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8: SEQ ID 12110; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 469 AA;
 SQ

Query Match 100.0%; Score 30; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 |||||
 Db 214 plglar 219

RESULT 10
 AAB92882
 ID AAB92882 standard; Protein; 484 AA.
 AC
 XX AAB92882;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:11481.
 DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.

XX (HELI-) HELIX RES INST.
PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
DR
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 11481; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 484 AA:

Query Match 100.0%; Score 30; DB 22; Length 484;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plqgar 6
|||||
Db 209 plqgar 214

RESULT 11
AAB18971
ID AAB18971 standard; Protein; 489 AA.
XX
AC AAB18971;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of a human transmembrane protein.
XX
KW Human; transmembrane protein; cell proliferation disorder; myeloma;
KW reproductive disorder; smooth muscle disorder; neurological disorder;
KW arteriosclerosis; leukaemia; acquired immunodeficiency syndrome; AIDS;
KW allergy; ovulatory defect; angina; hypertension; stroke; epilepsy;
KW Alzheimer's disease; Tourette's disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 10
FT /note= "potential phosphorylation site"
FT Modified-site 51
FT /note= "potential phosphorylation site"

FT Modified-site 52
FT /note= "potential phosphorylation site"
FT Modified-site 105
FT /note= "potential glycosylation site"
FT Modified-site 121
FT /note= "potential glycosylation site"
FT Modified-site 135
FT /note= "potential phosphorylation site"
FT Modified-site 143
FT /note= "potential phosphorylation site"
FT Modified-site 185
FT /note= "potential phosphorylation site"
FT Modified-site 224
FT /note= "potential phosphorylation site"
FT Modified-site 244
FT /note= "potential phosphorylation site"
FT Modified-site 252
FT /note= "potential phosphorylation site"
FT Region 263..284
FT /note= "leucine zipper"
FT Modified-site 279
FT /note= "potential phosphorylation site"
FT Modified-site 291
FT /note= "potential phosphorylation site"
FT Modified-site 379
FT /note= "potential phosphorylation site"
FT Region 399..420
FT /note= "leucine zipper"
FT Modified-site 416
FT /note= "potential phosphorylation site"
FT Modified-site 483
FT /note= "potential phosphorylation site"
XX WO200056891-A2.
XX
PD 28-SEP-2000.
XX
XX 22-MAR-2000; 2000WO-US07817.
XX
PR 22-MAR-1999; 99US-0125537.
PR 16-JUN-1999; 99US-0139565.
XX
XX (INCY-) INCYTE PHARM INC.
PA
PI Yue H, Lal P, Tang YT, Hillman JL, Reddy R, Bandman O, Baughn MR;
PI Lu DAM, Azimzai Y, Yang J;
XX
XX WPI; 2000-579485/54.
DR N-PSDB; AAA96484.
XX
PT New human transmembrane proteins are used to treat a disease or
PT condition associated with decreased expression of functional HTMP e.g.
PT Tourette's disorder, angina and leukaemia -
XX
PS Claim 1; Page 92-93; 130pp; English.
XX
CC The present sequence represents a human transmembrane proteins (HTMP).
CC Agonists and antagonists of the protein are used to treat a disease
CC or condition associated with overexpression of the protein. Diseases
CC and conditions which can be treated include cell proliferative,
CC immunological, reproductive, smooth muscle and neurological disorders
CC e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency
CC syndrome (AIDS), allergies, ovulatory defects, angina, hypertension,
CC stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The
CC polynucleotides may be used to detect and quantify gene expression in
CC biopsied tissues where protein expression may be correlated with disease
CC e.g. to determine absence, presence or excess expression of HTMP or to
CC monitor regulation of HTMP expression during therapeutic intervention.
XX
SQ Sequence 489 AA:

Query Match 100.0%; Score 30; DB 21; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 214 plglar 219

RESULT 12
AAY66660
ID AAY66660 standard; protein; 489 AA.
XX AAY66660;
AC AAY66660;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO783.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.

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PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AA264989.
XX
PT Membrane-bound proteins and related nucleotide sequences
XX
PS claim 12; Fig 79; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 489 AA;

Query Match 100.0%; Score 30; DB 21; Length 489;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 214 plglar 219
|||||

RESULT 13
AAM38703
ID AAM38703 standard; Protein; 489 AA.
XX
AC AAM38703;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 1848.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
KW
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Tang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI57859.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
Example 3; SEQ ID NO 1848; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 489 AA;

Query Match 100.0%; Score 30; DB 22; Length 489;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 214 plglar 219
|||||

RESULT 14
AAB65183
ID AAB65183 standard; Protein; 489 AA.
XX
AC AAB65183;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO783 (UNQ458) protein sequence SEQ ID NO:138.
XX
```

KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.

OS Homo sapiens.

XX WO200073454-A1.

PN 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 08-OCT-1999; 99US-0158663.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 02-MAR-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Grietsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kijavlin IL, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI; 2001-032160/04.

XX N-PSDB; AAF44135.

XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 79; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytostatic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA

CC and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in

CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and

CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 489 AA;

XX Query Match 100.0%; Score 30; DB 22; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglar 6

Db 214 plglar 219

RESULT 15

AAM40489

ID AAM40489 standard; Protein; 538 AA.

XX AAM40489;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 5420.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI59645.

XX Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

XX Example 2; SEQ ID NO 5420; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

XX specification.

SQ Sequence 538 AA;

Query Match 100.0%; Score 30; DB 22; Length 538;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 281 plglar 286

Search completed: February 28, 2002, 16:47:04

Job time: 59 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 93.69 Seconds
(without alignments)
17.781 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	30	100.0	128	23	US-09-902-540-12523
4	30	100.0	177	21	US-09-758-472-5376
5	30	100.0	203	16	US-09-252-991A-19176
6	30	100.0	230	16	US-09-252-691-6030
7	30	100.0	230	16	US-09-252-691C-6030
8	30	100.0	277	1	PCT-US01-14827-12965
9	30	100.0	293	16	US-09-252-991A-19047

10	30	100.0	333	19	US-09-562-737-6	Sequence 6, Appli
11	30	100.0	362	1	PCT-US01-16450-2736	Sequence 2736, Ap
12	30	100.0	362	1	PCT-US01-16450A-2736	Sequence 2736, Ap
13	30	100.0	362	21	US-09-731-872-280	Sequence 280, App
14	30	100.0	362	22	US-09-876-997-280	Sequence 280, App
15	30	100.0	362	24	US-60-169-629-495	Sequence 495, App
16	30	100.0	362	24	US-60-187-470-495	Sequence 495, App
17	30	100.0	406	23	US-09-902-540-13528	Sequence 13528, A
18	30	100.0	469	18	US-09-488-725A-1849	Sequence 1849, Ap
19	30	100.0	485	16	US-09-252-991A-17683	Sequence 17683, A
20	30	100.0	489	18	US-09-488-725A-1848	Sequence 1848, Ap
21	30	100.0	489	21	US-09-709-238-138	Sequence 138, App
22	30	100.0	489	23	US-09-941-992-138	Sequence 138, App
23	30	100.0	489	24	US-60-125-537-8	Sequence 8, Appli
24	30	100.0	535	18	US-09-489-039A-13906	Sequence 13906, A
25	30	100.0	538	18	US-09-488-725A-5420	Sequence 5420, Ap
26	30	100.0	538	18	US-09-488-725A-5421	Sequence 5421, Ap
27	30	100.0	592	23	US-09-955-999-112	Sequence 112, App
28	30	100.0	635	16	US-09-252-991A-16721	Sequence 16721, A
29	28	93.3	38	7	US-08-344-185B-428	Sequence 428, App
30	28	93.3	38	7	US-08-344-185C-428	Sequence 428, App
31	28	93.3	182	16	US-09-252-691-9747	Sequence 9747, Ap
32	28	93.3	182	16	US-09-252-691C-9747	Sequence 9747, Ap
33	28	93.3	196	16	US-09-252-991A-18189	Sequence 18189, A
34	28	93.3	206	16	US-09-270-767-57749	Sequence 57749, A
35	28	93.3	206	16	US-09-270-849B-182867	Sequence 182867, A
36	28	93.3	273	16	US-09-252-991A-32405	Sequence 32405, A
37	28	93.3	357	16	US-09-270-767-42454	Sequence 42454, A
38	28	93.3	381	16	US-09-252-991A-28320	Sequence 28320, A
39	28	93.3	469	24	US-60-324-109-30092	Sequence 30092, A
40	28	93.3	478	24	US-60-312-544-10512	Sequence 10512, A
41	28	93.3	481	16	US-09-252-991A-23317	Sequence 23317, A
42	28	93.3	494	15	US-09-126-420A-26	Sequence 26, Appli
43	28	93.3	544	17	US-09-328-352-6896	Sequence 6896, App
44	28	93.3	676	24	US-60-258-275-375	Sequence 375, App
45	28	93.3	703	16	US-09-252-991A-18391	Sequence 18391, A

ALIGNMENTS

RESULT 1
US-09-464-908-1
; Sequence 1, Application US/09464908
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; TITLE OF INVENTION: Selective inhibitors of MMP-12
; FILE REFERENCE: HMR2026A
; CURRENT APPLICATION NUMBER: US/09/464,908
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/155,223
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-464-908-1

Query Match 100.0%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 1 PLGLAR 6

RESULT 2
US-09-588-417-6
; Sequence 6, Application US/09588417

; GENERAL INFORMATION:
; APPLICANT: Fourie, Anne
; APPLICANT: Karlsson, Lars
; APPLICANT: Thurmond, Rob
; TITLE OF INVENTION: Metalloprotease Peptide Substrates And Methods
; FILE REFERENCE: ORT-1220
; CURRENT APPLICATION NUMBER: US/09/588,417
; CURRENT FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-588-417-6

Query Match 100.0%; Score 30; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
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Db 2 PLGLAR 7

RESULT 3
US-09-902-540-12523
; Sequence 12523, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12523
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12523

Query Match 100.0%; Score 30; DB 23; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||
Db 77 PLGLAR 82

RESULT 4
US-09-758-472-5376
; Sequence 5376, Application US/09758472
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PH001
; CURRENT APPLICATION NUMBER: US/09/758,472
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 9632
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5376
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-472-5376

Query Match 100.0%; Score 30; DB 21; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
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Db 53 PLGLAR 58

RESULT 5
US-09-252-991A-19176
; Sequence 19176, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19176
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19176

Query Match 100.0%; Score 30; DB 16; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
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Db 130 PLGLAR 135

RESULT 6
US-09-252-691-6030
; Sequence 6030, Application US/09252691B
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252,691B
; CURRENT FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 11324
; SEQ ID NO 6030
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-09-252-691-6030

Query Match 100.0%; Score 30; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
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Db 96 PLGLAR 101

RESULT 7

US-09-252-691C-6030
; Sequence 6030, Application US/09252691C
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252.691C
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094.145
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: US 60/074.787
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 11326
; SEQ ID NO 6030
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-09-252-691C-6030

Query Match 100.0%; Score 30; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 96 PLGLAR 101

RESULT 8

PCT-US01-14827-12965
; Sequence 12965, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577.408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 12965
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-14827-12965

Query Match 100.0%; Score 30; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 153 PLGLAR 158

RESULT 9

US-09-252-991A-19047
; Sequence 19047, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19047
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19047

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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 89 PLGLAR 94

RESULT 10

US-09-562-737-6
; Sequence 6, Application US/09562737
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562.737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-6

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Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
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Db 2 PLGLAR 7

RESULT 11

PCT-US01-16450-2736
; Sequence 2736, Application PC/TUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205.515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450-2736

Query Match 100.0%; Score 30; DB 1; Length 362;

Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 87 PLGLAR 92

RESULT 12

PCT-US01-16450A-2736
; Sequence 2736, Application PC/TUS0116450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450A-2736

Query Match 100.0%; Score 30; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 87 PLGLAR 92

RESULT 13

US-09-731-872-280
; Sequence 280, Application US/09731872
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US3 REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 280
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-09-731-872-280

Query Match 100.0%; Score 30; DB 21; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 87 PLGLAR 92

RESULT 14

US-09-876-997-280
; Sequence 280, Application US/09876997
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US4 CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 280
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-09-876-997-280

Query Match 100.0%; Score 30; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 87 PLGLAR 92

RESULT 15

US-60-169-629-495
; Sequence 495, Application US/60169629
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: cDNAs for Secreted Proteins
; FILE REFERENCE: GENSET.071PRF
; CURRENT APPLICATION NUMBER: US/60/169,629
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 715
; SOFTWARE: Patent.pm
; SEQ ID NO 495
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-60-169-629-495

Query Match 100.0%; Score 30; DB 24; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 87 PLGLAR 92

Search completed: February 28, 2002, 16:49:23
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28; 2002, 16:46:05 ; Search time 14.33 Seconds
(without alignments)
23.705 Million cell update

Title: 09-876091
Perfect score: 30
Sequence: 1 plqlar

Scoring table: BLOSUM62
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Searched: 258822 seqs, 56616433 residues

Total number of hits satisfying chosen parameters: 258822

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	8		Length	DB	ID	Description
		Match	Query				
1	30	100.0	8	6	US-10-050-200-39	Sequence 39, Appl	
2	30	100.0	119	5	US-09-708-427-74176	Sequence 74176, A	
3	30	100.0	219	6	US-10-015-127-10477	Sequence 10477, A	
4	30	100.0	489	5	US-09-989-723-138	Sequence 138, App	
5	30	100.0	489	5	US-09-989-724-138	Sequence 138, App	
6	30	100.0	489	5	US-09-989-730-138	Sequence 138, App	
7	30	100.0	489	5	US-09-989-436-138	Sequence 138, App	
8	30	100.0	489	5	US-09-990-444-138	Sequence 138, App	
9	30	100.0	489	5	US-09-989-721-138	Sequence 138, App	
10	30	100.0	489	5	US-09-989-722-138	Sequence 138, App	
11	30	100.0	489	5	US-09-989-725-138	Sequence 138, App	
12	30	100.0	489	5	US-09-989-726-138	Sequence 138, App	
13	30	100.0	489	5	US-09-989-727-138	Sequence 138, App	
14	30	100.0	489	5	US-09-989-728-138	Sequence 138, App	
15	30	100.0	489	5	US-09-989-731-138	Sequence 138, App	
16	30	100.0	489	5	US-09-989-732-138	Sequence 138, App	
17	30	100.0	489	5	US-09-989-734-138	Sequence 138, App	
18	30	100.0	489	5	US-09-990-437-138	Sequence 138, App	
19	30	100.0	489	5	US-09-990-438-138	Sequence 138, App	
20	30	100.0	489	5	US-09-990-440-138	Sequence 138, App	
21	30	100.0	489	5	US-09-990-441-138	Sequence 138, App	
22	30	100.0	489	5	US-09-989-279-138	Sequence 138, App	
23	30	100.0	489	5	US-09-989-735-138	Sequence 138, App	
24	30	100.0	489	5	US-09-990-439-138	Sequence 138, App	
25	30	100.0	489	5	US-09-990-562-138	Sequence 138, App	
26	30	100.0	489	5	US-09-997-349-138	Sequence 138, App	

ALIGNMENTS

RESULT

```

US-10-050-200-39
:
: Sequence 39, Application US/100502000
: GENERAL INFORMATION:
: APPLICANT: Fourie, Anne
: APPLICANT: Cotes, Fawn
: APPLICANT: Karlsson, Lars
: TITLE OF INVENTION: Aggrucanase-1 a
: FILE REFERENCE: ORT-1417
: CURRENT APPLICATION NUMBER: US/10/0
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 39
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: peptide substr
: US-10-050-200-39

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Query Match	100.0%	Score 30;	DB 6;	Length 8;
Best Local Similarity	100.0%	Pred. No. 2.3e+05;		
Matched	Conservative	0.0	Microtear	Indole

Qy	1	plglar	6
Db	3	PLGLAR	8

RESULT

```

US-09-708-427-74176
; Sequence 74176, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED D
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708, 427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74176
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: 1..119
; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..119
; OTHER INFORMATION: Ceres Seq. ID 1945018
US-09-708-427-74176

Query Match 100.0%; Score 30; DB 5; Length 119;

Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 66 PLGLAR 71

RESULT 3

US-10-015-127-10477
; Sequence 10477, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Spingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 10477
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Spingomonas elodea
US-10-013-127-10477

Query Match 100.0%; Score 30; DB 6; Length 219;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 63 PLGLAR 68

RESULT 4

US-09-989-723-138
; Sequence 138, Application US/09989723
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088876
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plglar 6
|||||
Db 214 PLGLAR 219

RESULT 5
US-09-989-724-138
; Sequence 138, Application US/09989724
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC67
; CURRENT APPLICATION NUMBER: US/09/989, 724
; CURRENT FILING DATE: 2001-11-20

;	PRIOR FILING DATE:	1998-06-12	
;	PRIOR APPLICATION NUMBER:	60/089440	
;	PRIOR FILING DATE:	1998-06-16	
;	PRIOR APPLICATION NUMBER:	60/089512	
;	PRIOR FILING DATE:	1998-06-16	
;	PRIOR APPLICATION NUMBER:	60/089514	
;	PRIOR FILING DATE:	1998-06-16	
;	PRIOR APPLICATION NUMBER:	60/089532	
;	PRIOR FILING DATE:	1998-06-17	
;	PRIOR APPLICATION NUMBER:	60/089538	
;	PRIOR FILING DATE:	1998-06-17	
;	PRIOR APPLICATION NUMBER:	60/089598	
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;	PRIOR APPLICATION NUMBER:	60/090444	
;	PRIOR FILING DATE:	1998-06-24	
;	PRIOR APPLICATION NUMBER:	60/090445	
;	PRIOR FILING DATE:	1998-06-24	
;	PRIOR APPLICATION NUMBER:	60/090472	
;	PRIOR FILING DATE:	1998-06-24	
;	PRIOR APPLICATION NUMBER:	60/090535	
;	PRIOR FILING DATE:	1998-06-24	
;	PRIOR APPLICATION NUMBER:	60/090540	
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;	PRIOR APPLICATION NUMBER:	60/090542	
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;	PRIOR FILING DATE:	1998-06-24	
;	PRIOR APPLICATION NUMBER:	60/090676	
;	PRIOR FILING DATE:	1998-06-25	
;	PRIOR APPLICATION NUMBER:	60/090678	
;	PRIOR FILING DATE:	1998-06-25	
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;	PRIOR APPLICATION NUMBER:	60/090696	
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; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6

Db 214 PLGLAR 219

RESULT 6

US-09-989-730-138

; Sequence 138, Application US/09989730

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C69
 ; CURRENT APPLICATION NUMBER: US/09/989,730
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
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 ; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 214 PLGLAR 219

RESULT 7

US-09-990-436-138

; Sequence 138, Application US/09990436

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavir, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC14

; CURRENT APPLICATION NUMBER: US/09/990,436

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 214 PLGLAR 219
|||||

RESULT 8

US-09-990-444-138

; Sequence 138. Application US/09990444

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC19

; CURRENT APPLICATION NUMBER: US/09/990,444

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18

b6.

;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
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;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 214 PLGLAR 219
|||||

RESULT 9
US-09-989-721-138
; Sequence 138, Application US/09989721
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989, 721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels

Qy 1 plglar 6
Db 214 PLGLAR 219

RESULT 10

US-09-989-722-138
; Sequence 138, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989, 722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 214 PLGLAR 219

RESULT 1*

US-09-989-725-138

;; Sequence 138, Application US/09989725
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C71
;; CURRENT APPLICATION NUMBER: US/09/989,725
;; CURRENT FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 214 PLGLAR 219

RESULT 12
US-09-989-726-138
; Sequence 138, Application US/09989726
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6

Db 214 PLGLAR 219
|||||

RESULT 13

US-09-989-727-138

; Sequence 138, Application US/09989727

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hauspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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;; PRIOR APPLICATION NUMBER: 60/088738
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;; PRIOR APPLICATION NUMBER: 60/090472
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plqlar 6

Db 214 plqlar 219

RESULT 14

US-09-989-728-138

;; Sequence 138, Application US/09989728

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
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;; PRIOR APPLICATION NUMBER: 60/090678
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;

Qy 1 p1glar 6

Db 214 PLGLAR 219

RESULT 15

US-09-989-731-138
Sequence 138, Application US/09989731

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumes, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

;; FILE REFERENCE: P2730PIC70
;; CURRENT APPLICATION NUMBER: US/09/989,731
;; PRIOR FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695

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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 214 PLGLAR 219

Search completed: February 28, 2002, 16:49:44
Job time: 219 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 12.48 seconds
(without alignments)
10.819 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	77	4	US-09-246-500B-2
2	28	93.3	422	2	US-08-403-852D-17
3	28	93.3	422	3	US-08-510-646B-18
4	28	93.3	422	4	US-09-231-818-17
5	27	90.0	275	4	US-08-976-255-16
6	27	90.0	472	4	US-08-976-255-17
7	26	86.7	568	1	US-08-262-424-7
8	26	86.7	568	2	US-08-493-197-7
9	26	86.7	568	3	US-08-717-587A-4
10	26	86.7	568	3	US-08-883-610A-4
11	26	86.7	568	4	US-08-936-094A-4
12	26	86.7	568	5	PCT-US95-07844-7
13	25	83.3	15	2	US-08-368-834-14
14	25	83.3	15	2	US-08-447-154-14
15	25	83.3	16	3	US-09-136-251-6
16	25	83.3	70	4	US-08-965-056-93
17	25	83.3	84	4	US-08-905-223-404
18	25	83.3	104	4	US-08-965-056-91
19	25	83.3	114	2	US-08-473-020A-21
20	25	83.3	114	2	US-08-473-020A-22
21	25	83.3	114	2	US-08-473-020A-23
22	25	83.3	114	2	US-08-473-020A-26
23	25	83.3	114	2	US-08-473-020A-27
24	25	83.3	120	2	US-08-997-080-80
25	25	83.3	120	2	US-08-997-362-80
26	25	83.3	120	3	US-08-873-970-80
27	25	83.3	120	4	US-09-095-855-80

28	83.3	122	2	US-08-473-020A-25	Sequence 25, Appl
29	83.3	198	4	US-08-965-056-90	Sequence 90, Appl
30	83.3	215	2	US-08-997-080-117	Sequence 117, App
31	83.3	215	2	US-08-997-362-117	Sequence 117, App
32	83.3	215	4	US-09-095-855-117	Sequence 117, App
33	83.3	240	4	US-08-913-014A-1	Sequence 1, Appli
34	83.3	267	1	US-08-570-929-2	Sequence 2, Appli
35	83.3	269	3	US-08-759-463-2	Sequence 2, Appli
36	83.3	269	4	US-09-328-153-2	Sequence 2, Appli
37	83.3	286	4	US-09-188-930-137	Sequence 137, App
38	83.3	299	4	US-08-944-483-66	Sequence 66, Appl
39	83.3	301	1	US-08-420-235B-47	Sequence 47, Appl
40	83.3	301	2	US-08-343-101A-22	Sequence 22, Appl
41	83.3	301	3	US-09-183-688-22	Sequence 22, Appl
42	83.3	301	4	US-08-793-624-47	Sequence 47, Appl
43	83.3	355	4	US-09-194-905-10	Sequence 10, Appl
44	83.3	389	2	US-08-485-449-6	Sequence 6, Appli
45	83.3	422	4	US-09-151-102-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-246-500B-2
; Sequence 2, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; TITLE OF INVENTION: Using the Substrates
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246.500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Pig C3a Anaphylatoxin
US-09-246-500B-2

Query Match 100.0%; Score 30; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 72 PLGLAR 77

RESULT 2
US-08-403-852D-17
; Sequence 17, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-852D-17

Query Match 93.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 188 PLGIAR 193

RESULT 3
US-08-510-646B-18
Sequence 18, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-18

Query Match 93.3%; Score 28; DB 3; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 188 PLGIAR 193

RESULT 4
US-09-231-818-17
Sequence 17, Application US/09231818
Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-17

Query Match 93.3%; Score 28; DB 4; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 188 PLGIAR 193

RESULT 5
US-08-976-255-16
Sequence 16, Application US/08976255
Patent No. 6136581
GENERAL INFORMATION:
APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-976-255-16

Query Match 90.0%; Score 27; DB 4; Length 275;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 60 PLGLSR 65

RESULT 6
US-08-976-255-17
Sequence 17, Application US/08976255
Patent No. 6136581
GENERAL INFORMATION:
APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-976-255-17

Query Match 90.0%; Score 27; DB 4; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 125 PLGLSR 130

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RESULT 7
US-08-262-424-7
; Sequence 7, Application US/08262424
; Patent No. 5604111
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalate
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-424-7

Query Match 86.7%; Score 26; DB 1; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 146 PIGIAR 151

RESULT 8
US-08-493-197-7
; Sequence 7, Application US/08493197
; Patent No. 5837833
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalate
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/493,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-493-197-7

Query Match 86.7%; Score 26; DB 2; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 146 PIGIAR 151

RESULT 9
US-08-717-587A-4
; Sequence 4, Application US/08717587A
; Patent No. 5912125
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalobacter
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,587A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/493,197
; FILING DATE: 20-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: UF-145C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
```

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-587A-4

Query Match 86.7%; Score 26; DB 2; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 146 PIGIAR 151

RESULT 10

US-08-883-610A-4
Sequence 4, Application US/08883610A
Patent No. 6050628

GENERAL INFORMATION:
APPLICANT: Peck, Ammon B.
APPLICANT: Sidhu, Harmeet
TITLE OF INVENTION: Materials and Methods for Detection of
TITLE OF INVENTION: Oxalobacter
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,610A
FILING DATE: 26-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/717,587
FILING DATE: 27-SEP-1996
CLASSIFICATION:
APPLICATION NUMBER: US 08/493,197
FILING DATE: 20-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: US 08/262,424
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: UF-145C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-610A-4

Query Match 86.7%; Score 26; DB 3; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 146 PIGIAR 151

RESULT 11

US-08-936-094A-4
Sequence 4, Application US/08936094A
Patent No. 6214980

GENERAL INFORMATION:
APPLICANT: Peck, Ammon B.
APPLICANT: Sidhu, Harmeet
TITLE OF INVENTION: Materials and Methods for Detection of Oxalobacter formigenes
FILE REFERENCE: UF-145C4
CURRENT APPLICATION NUMBER: US/08/936,094A
CURRENT FILING DATE: 1997-09-23
PRIOR APPLICATION NUMBER: 08/883,610
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: 08/717,587
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 08/493,197
PRIOR FILING DATE: 1995-06-20
PRIOR APPLICATION NUMBER: 08/262,424
PRIOR FILING DATE: 1994-06-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in version 3.0
SEQ ID NO 4
LENGTH: 568
TYPE: PRT
ORGANISM: Oxalobacter formigenes
US-08-936-094A-4

Query Match 86.7%; Score 26; DB 4; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 146 PIGIAR 151

RESULT 12

PCT-US95-07844-7
Sequence 7, Application PC/TUS9507844
GENERAL INFORMATION:

APPLICANT:
APPLICANT: Street address: 223 Grinter Hall
APPLICANT: City: Gainesville
APPLICANT: State/Province: Florida
APPLICANT: Country: US
APPLICANT: Postal code/zip: 32611
APPLICANT: Phone number: 904-392-8929
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for Detection of
TITLE OF INVENTION: Oxalate
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606

Fax number: 904-392-6600

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/07844
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/262,424
;; FILING DATE: 20-JUN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: UFI45
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 568 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; PCT-US95-07844-7

Query Match 86.7%; Score 26; DB 5; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
I:|:|
Db 146 PIGIAR 151

RESULT 13
US-08-368-834-14
; Sequence 14, Application US/08368834
; Patent No. 5874405
; GENERAL INFORMATION:
; APPLICANT: Birnbaum, Gary
; APPLICANT: Kotilinek, Linda K.
; TITLE OF INVENTION: Heat Shock Protein Peptides That Share
; TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase and
; TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous System
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5874405west Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,834
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.3030501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-07844-7

;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-368-834-14

Query Match 83.3%; Score 25; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plglar 6
I:|:|
Db 2 PLGLKR 7

RESULT 14
US-08-447-154-14
; Sequence 14, Application US/08447154
; Patent No. 5958416
; GENERAL INFORMATION:
; APPLICANT: Birnbaum, Gary
; APPLICANT: Kotilinek, Linda K.
; TITLE OF INVENTION: Heat Shock Protein Peptides That
; TITLE OF INVENTION: Share
; TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous
; TITLE OF INVENTION: System
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5958416west Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,154
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/368,834
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.3090501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-447-154-14

Query Match 83.3%; Score 25; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglar 6
| | | | |
Db 2 PLGLKR 7

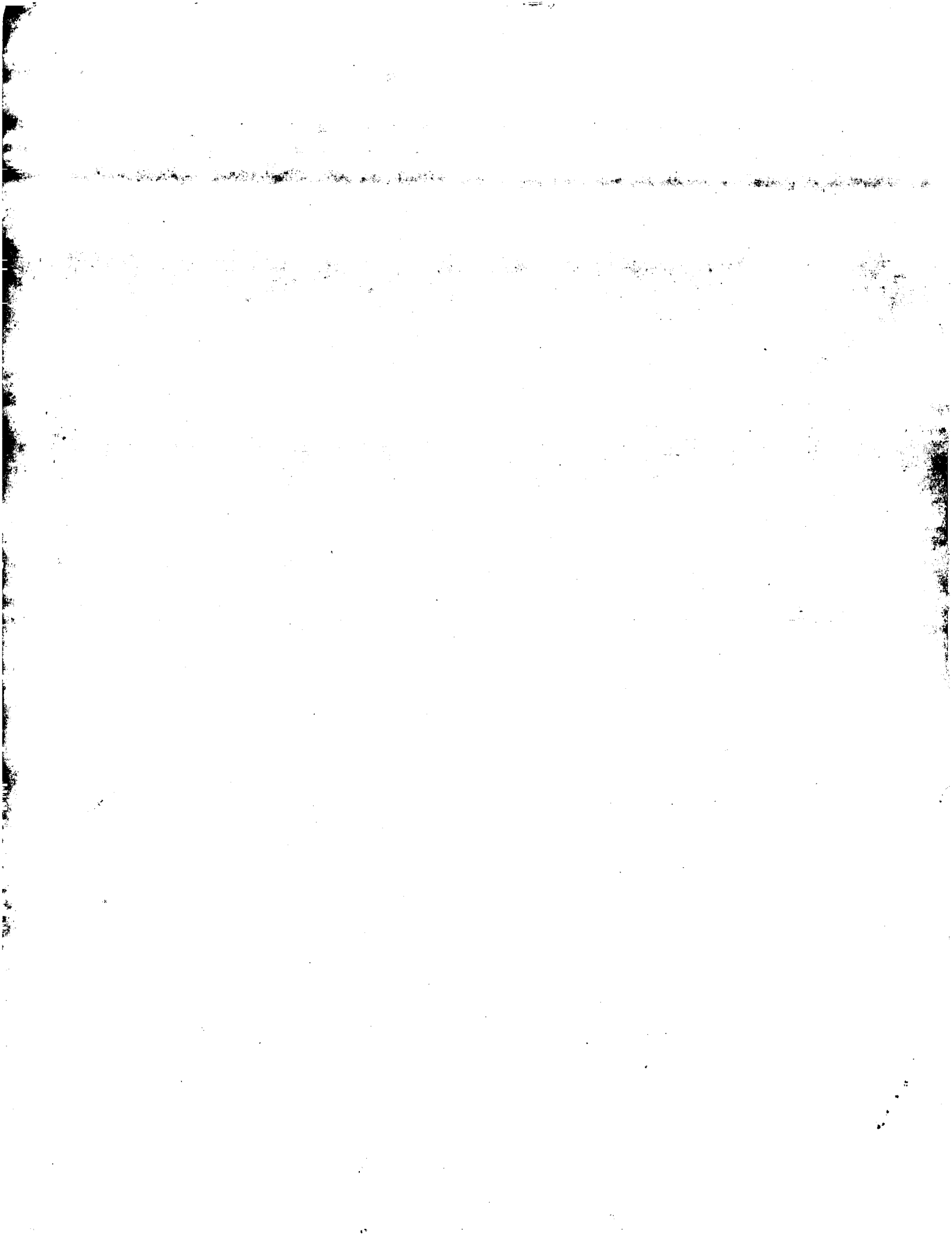
RESULT 15

US-09-136-251-6
; Sequence 6, Application US/09136251A
; Patent No. 6127156
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6127156ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/136,251A
; CURRENT FILING DATE: 1998-08-19
; EARLIER APPLICATION NUMBER: EP 97114432.4
; EARLIER FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (13)
US-09-136-251-6

Query Match 83.3%; Score 25; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglar 6
| | | | |
Db 7 PLGTAR 12

Search completed: February 28, 2002, 16:47:42
Job time: 97 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:49:45 ; Search time 12.68 Seconds
(without alignments)
36.045 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 315

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	56.7	4	2 A32039	tyrosine-melanocyt
2	13	43.3	5	2 A44955	alkanal monooxygen
3	11	36.7	4	2 I61883	protamine pl - ora
4	11	36.7	4	2 I37013	protamine pl - Cer
5	11	36.7	4	2 I84439	protamine pl - sav
6	11	36.7	5	2 I39964	ribosomal protein
7	11	36.7	5	2 I39966	ribosomal protein
8	11	36.7	5	2 I39965	ribosomal protein
9	11	36.7	5	2 G44817	27.5 kda structura
10	11	36.7	5	2 I44817	27.5K structural p
11	11	36.7	5	2 E44817	27.5K structural p
12	11	36.7	5	2 C44817	28.5K structural p
13	11	36.7	5	2 A44817	28K structural pro
14	11	36.7	6	2 I37027	protamine pl - gor
15	11	36.7	6	2 PT0568	T-cell receptor be
16	10	33.3	4	2 S18401	thyroglobulin - do
17	10	33.3	4	2 I38888	CoI intron 16 prot
18	10	33.3	4	2 A32480	achatin-I - giant
19	10	33.3	4	2 PT0240	Ig heavy chain CRD
20	10	33.3	4	2 A53284	T-cell receptor be
21	10	33.3	4	2 PT0721	T-cell receptor be
22	10	33.3	5	2 D44823	synaptosomal-assoc
23	10	33.3	5	2 PT0713	T-cell receptor be
24	10	33.3	6	2 S11024	hydrogensulfite re
25	10	33.3	6	2 B56979	collagen alpha 1(I
26	10	33.3	6	2 H48394	glycoprotein compo
27	10	33.3	6	2 A20186	fatty-acid synthas
28	10	33.3	6	2 PT0643	T-cell receptor be
29	10	33.3	6	2 PT0621	T-cell receptor be

30	10	33.3	6	2 PT0560	T-cell receptor be
31	10	33.3	6	2 PT0718	T-cell receptor be
32	10	33.3	6	2 PT0589	T-cell receptor be
33	10	33.3	6	2 PT0727	T-cell receptor be
34	10	33.3	6	2 PT0730	T-cell receptor be
35	9	30.0	3	2 PQ0010	angiotensin-conver
36	9	30.0	5	2 E60274	major protein anti
37	9	30.0	5	2 S51077	alpha-amylase - ri
38	9	30.0	5	2 B37988	acid proteinase li
39	9	30.0	5	2 S62883	seminal plasma pro
40	9	30.0	6	2 A35890	RNA-directed DNA p
41	9	30.0	6	2 A61049	halo-toxin - Pseud
42	9	30.0	6	2 PQ0008	angiotensin-conver
43	9	30.0	6	2 A27696	contraction-inhibi
44	9	30.0	6	2 B27696	contraction-inhibi
45	8	26.7	3	2 B23751	spinal cord peptid

ALIGNMENTS

RESULT 1

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C:Accession: A32039

R:Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact

A:Reference number: A32039; MUID:89123285

A:Accession: A32039

A:Molecule type: protein

A:Residues: 1-4 <HOR>

A:Experimental source: brain

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end

F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 56.7%; Score 17; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3

Db 2 PLG 4

RESULT 2

A44955

alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragm

C:Species: Vibrio harveyi

C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000

C:Accession: A44955

R:Paquette, O.; Tu, S.C.

Photochem. Photobiol. 50, 817-825, 1989

A:Title: Chemical modification and characterization of the alpha cysteine 106 at the

A:Reference number: A44955; MUID:90175700

A:Accession: A44955

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <PAQ>

C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match

Best Local Similarity 43.3%; Score 13; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 glar 6

Db 2 GIXR 5

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RESULT 3
I61883
protamine P1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I61883
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I61883
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 4
I37013
protamine P1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I37013
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I37013
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 5
I84439
protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doguera (savannah baboon)
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I84439
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I84439
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12147; NID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 6
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39964
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:g143471
C:Genetics:
A:Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 7
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39966
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:g143475
C:Genetics:
A:Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 8
I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39965
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
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A;Accession: I39965
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99042; NID:g143473
C;Genetics:
A;Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lgl 6
:||
Db 1 MAR 3

RESULT 9

G44817
27.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C;Species: Leuconostoc oenos phase P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: G44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: G44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 10

I44817
27.5K structural protein - Leuconostoc oenos phase P37 (fragment)
C;Species: Leuconostoc oenos phase P37
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: I44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: I44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 11

E44817
27.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C;Species: Leuconostoc oenos phase P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C;Accession: E44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: E44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 12

C44817
28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)
C;Species: Leuconostoc oenos phase PAT5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: C44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: C44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 13

A44817
28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)
C;Species: Leuconostoc oenos phase PZt11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: A44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: A44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 14

I37027
protamine P1 - gorilla (fragment)

C:Species: Gorilla gorilla (gorilla)
 C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
 C:Accession: I37027
 R:Queralt, R.; Oliva, R.
 Gene 133, 197-204, 1993
 A:Title: Identification of conserved potential regulatory sequences of the protamine-end
 A:Reference number: I37013; MUID:94040810
 A:Accession: I37027
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-6 <RES>
 A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 36.7%; Score 11; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
 :||
 Db 1 MAR 3

RESULT 15

PT0568
 T-cell receptor beta chain V-D-J region (141-1C) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0568
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0568
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 36.7%; Score 11; DB 2; Length 6;
 Best Local Similarity 75.0%; Pred. No. 2.2e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 glar 6
 :||
 Db 3 GDAR 6

Search completed: February 28, 2002, 16:51:38
 Job time: 113 sec

herpes simplex virus (type 1) (strain KOS).
 Viruses: dsDNA viruses, no RNA stage: Herpesviridae:

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OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation. -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57646; AAA45830.1; -
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 pl 2
Db 5 PL 6

RESULT 3
ACH1_ACHFU
ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ACHATIN-I.
OS Achatina fullica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=FERUSSAC; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fullica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fullica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;

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RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT D-amino acid residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR PIR; A32480; A32480.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 33.3%; Score 10; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 gla 5
Db 1 GFA 3

RESULT 4
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5 5 AMIDATION (POTENTIAL).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 33.3%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 gl 4
Db 4 GL 5

RESULT 5
TMOF_SARBU
ID TMOF_SARBU STANDARD; PRT; 6 AA.
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE TRYPSTIN-MODULATING OOSTATIC FACTOR (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Sarcophagidae; Sarcophaga.

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OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic
 RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 RT (Sarcophaga) bullata";
 RL Regul. Pept. 50:61-72(1994).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 33.3%; Score 10; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

Qy 1 plgl 4
 Db 2 PTNL 5

RESULT 6
 CIP1_MYTED
 ID CIP1_MYTED STANDARD; PRT; 6 AA.
 AC P13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CONTRACTION-INHIBITING PEPTIDE I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RA "Structures and actions of Mytilus inhibitory peptides";
 RT Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 RL -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP II.
 CC PIR: A27696; A27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 30.0%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 pl 2
 Db 3 PM 4

RESULT 7
 CIP2_MYTED
 ID CIP2_MYTED STANDARD; PRT; 6 AA.
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CONTRACTION-INHIBITING PEPTIDE II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RA "Structures and actions of Mytilus inhibitory peptides";
 RT Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 RL -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 CC PIR: B27696; B27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 30.0%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 pl 2
 Db 3 PM 4

RESULT 8
 DCML_PSECH
 ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RA "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrophic bacteria";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
 CC ACCEPTOR.
 CC -!- COFACTOR: MOLYBDENUM.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: PL0140; PL0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 lq 3
 Db 1 MG 2

RESULT 9
 DCMS_PSECH
 ID DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;

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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=290;
RN [1]
RN SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
  carboxydohydrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
  ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
  SMALL.
DR PIR; PLO146; PLO146.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 4;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
DB 1 MAK 3

RESULT 10
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
  using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
  NON_TER 5
FT PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3
DB 2 IG 3

RESULT 11
THYL_PIG STANDARD; PRT; 3 AA.
ID THYL_PIG
AC P01151.

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE THYROLIBERIN (THYROTROPIN RELEASING HORMONE) (TRH).
OS Sus scrofa (Pig); Ovis aries (Sheep);
OS Bombina orientalis (Oriental fire-bellied toad), and
OC Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RN SEQUENCE.
RP SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106(1970).
RN [2]
RN SEQUENCE.
RP SPECIES=Pig;
RX MEDLINE=70039904; PubMed=4982117;
RA Boler J., Enzmann F., Folkers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
  releasing hormone and pyroglutanyl-histidyl-proline amide.";
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RN SEQUENCE.
RP SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
  Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
  stimulating hormone releasing factor of ovine origin by means of mass
  spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]
RN SEQUENCE.
RP SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
  Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic
  TSH-releasing factor.";
RL Nature 226:321-325(1970).
RN [5]
RN SEQUENCE.
RP SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RN SEQUENCE.
RP SPECIES=N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
  viridescens) brain in vitro. Isolation and characterization of
  thyrotropin releasing factor.";
RL J. Neurochem. 23:471-478(1974).
CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
  IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
  NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
CC PIR; A01415; RHPGT.
DR PIR; A93750; RHSHT.
DR PIR; A90919; RHTDFO.
DR PIR; A92971; A92971.
KW Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 3;

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Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
Db 3 p 3

RESULT 12
EESI_HUMAN
ID EESI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSINOPHILOACTIC PEPTIDES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS; THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PTR: A03190; ETHUL.
DR VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT
SQ SEQUENCE 4 AA; 390 MW; 68058862A0000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. le+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3
Db 1 VG 2

RESULT 13
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L1 (YML1) (FRAGMENT).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
DR PTR: S17255; S17255.
DR SGD: L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4

Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
Db 4 p 4

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
Db 4 p 4

RESULT 14
TUFT_HUMAN
ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFTSIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS; AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PTR: A02147; A02147.
DR MIM: 191150; -.
DR SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
Db 3 p 3

RESULT 15
BPP7_BOTIN
ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
```

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RL peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR; G37196; G37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
 Db 5 p 5

Search completed: February 28, 2002, 16:54:52
 Job time: 212 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:51:05 ; Search time 22.14 Seconds
(without alignments)
39.640 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	30.0	5	13	P82099 litoria rub
2	9	30.0	6	13	P82096 litoria rub
3	8	26.7	6	10	P82181 spinacia ol
4	8	26.7	6	10	P82182 spinacia ol
5	7	23.3	5	13	P82073 litoria rub
6	6	20.0	5	10	Q99007 hordeum vul
7	5	16.7	6	10	P82541 spinacia ol
8	4	13.3	4	11	Q08433 rattus norv
9	4	13.3	5	13	P82070 litoria rub
10	4	13.3	5	13	P82071 litoria rub
11	4	13.3	6	4	Q08720 homo sapien
12	2	6.7	5	13	P82072 litoria rub
13	2	6.7	5	13	P82100 litoria rub

ALIGNMENTS

RESULT 1

P82099 ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;
AMIDATION
Query Match 30.0%; Score 9; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 pl 2
Db 4 PM 5
RESULT 2
P82096 ID P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
AMIDATION
Query Match 30.0%; Score 9; DB 13; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 pl 2
Db 3 PI 4
RESULT 3
P82181 ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;

DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10_eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 26.7%; Score 8; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 4.7e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 lar 6
Db 2 ISR 4

RESULT 4
P82182 ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10_eub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 26.7%; Score 8; DB 10; Length 6;
Best Local Similarity 33.3%; Pred. No. 4.7e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 lar 6
Db 2 ISR 4

RESULT 5
P82073 ID P82073 PRELIMINARY; PRT; 5 AA.
AC P82073;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A0A0000 CRC64;

Query Match 23.3%; Score 7; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 lg 3
Db 1 VG 2

RESULT 6
Q99007 ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
OS AMYL.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Trillaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL: X54643; CAA38455.1; -.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 la 5
: 1
Db 1 MA 2

RESULT 7
P82541 ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435797; PubMed=10874039;
RT Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR002222; Ribosomal_S19.
DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMALS19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 732 MW; 6333735A411C0000 CRC64;

Query Match 16.7%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 r 6
: 1
Db 2 R 2

RESULT 8
Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDP-GT)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSOME.
EMBL: S38636; AAB19259.1; -.
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 13.3%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 l 2
: 1
Db 3 L 3

RESULT 9
P82070 ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinhilber S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 a 5

Db 5 A 5

RESULT 10

P82071 ID P82071 PRELIMINARY; PRT; 5 AA.
AC P82071; (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 A 5
Db 5 A 5

RESULT 11

Q08720 ID Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons.";
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1;
FT NON_TER 1 1
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1 2
Db 2 1 2

RESULT 12

P82072 ID P82072 PRELIMINARY; PRT; 5 AA.
AC P82072;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
DE RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 6.7%; Score 2; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 1 2
Db 1 1 1

RESULT 13

P82100 ID P82100 PRELIMINARY; PRT; 5 AA.
AC P82100;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
DE ELECTIN 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 6.7%; Score 2; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;

Matches	0;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	1	2						
Db	2	1	2						

Search completed: February 28, 2002, 16:54:35
Job time: 210 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:45 ; Search time 23.61 Seconds
(without alignments)
18.824 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 34718

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
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10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
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20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	18	3-methylcholanthrene
2	30	100.0	6	19	Matrix metallopro
3	25	83.3	6	5	Sequence of synthe
4	25	83.3	6	21	Collagenase substr
5	23	76.7	6	20	Non-crosslinked pr
6	23	76.7	6	21	Peptide sequencing
7	23	76.7	6	21	Collagenase substr
8	21	70.0	4	4	Substrate for coll
9	21	70.0	4	4	Peptide conjugated
10	21	70.0	4	19	Peptide-lipid conf
11	21	70.0	4	22	

12	21	70.0	6	5	Sequence of synthe
13	21	70.0	6	18	Recombinant human
14	21	70.0	6	21	Peptide linker #10
15	21	70.0	6	21	Matrix metalloprot
16	21	70.0	6	21	Matrix metalloprot
17	21	70.0	6	21	Thiopeptolide subs
18	21	70.0	6	21	Collagenase substr
19	21	70.0	6	22	Amino acid sequenc
20	21	70.0	6	22	AMP-2 protease cle
21	21	70.0	6	22	MTI-MMP protease c
22	21	70.0	6	22	Thiopeptolide subs
23	21	70.0	6	22	Thiopeptolide amin
24	21	70.0	6	22	Thiopeptolide. Un
25	21	70.0	6	22	Matrix metalloprot
26	21	70.0	6	22	Collagenase cleava
27	21	70.0	6	22	Peptide having opi
28	19	63.3	5	15	C5a anaphylatoxin-
29	19	63.3	6	15	Immobilised peptid
30	19	63.3	6	20	Collagenase substr
31	19	63.3	6	21	Collagenase derive
32	19	63.3	6	22	Sequence of peptid
33	18	60.0	6	5	Substrate #1 for m
34	18	60.0	6	18	Peptide #2 charact
35	18	60.0	6	20	Collagenase derive
36	18	60.0	6	21	Melanocyte stimula
37	18	60.0	6	22	Peptide for use in
38	17	56.7	3	22	Enzyme activity de
39	17	56.7	4	2	Insulin and secret
40	17	56.7	4	2	Substrate for coll
41	17	56.7	4	3	Sequence of the re
42	17	56.7	4	4	Melanotrophic rele
43	17	56.7	4	6	Melanotrophic rele
44	17	56.7	4	16	
45	17	56.7	4	16	

ALIGNMENTS

RESULT	1				
AA1980	1				
AA1981	1				
AA1982	1				
AA1983	1				
AA1984	1				
AA1985	1				
AA1986	1				
AA1987	1				
AA1988	1				
AA1989	1				
AA1990	1				
AA1991	1				
AA1992	1				
AA1993	1				
AA1994	1				
AA1995	1				
AA1996	1				
AA1997	1				
AA1998	1				
AA1999	1				
AA2000	1				
AA2001	1				

XX Zook SE, Dagnino R, Deason ME, Bender SL, Melnick MJ;
 XX WPI; 1997-332465/30.
 XX
 PT New N-hydroxy-benzenesulphonyl carboxamide derivatives - are
 PT metallo-protease inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 XX Example 22; Page 108; 151pp; English.
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. N-hydroxy benzenesulphonyl (thiazine or piperazine)
 CC carboxamide derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 2
 AAW52139
 ID AAW52139 standard; Peptide; 6 AA.
 XX
 AC AAW52139;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Matrix metalloproteinase MMP-9 substrate B.
 XX
 KW Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;
 KW metalloproteinase 12; MMP-12; osteoclastic proteinase;
 KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;
 KW bone resorption; metastasis; tumour; cancer; ulcer; arthritis;
 KW periodontal disease; therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Mca-proline"
 FT Cleavage-site 3..4
 FT Modified-site 5
 FT /note= "Dpa-alanine"
 XX
 PN WO9804287-A1.
 XX
 PD 05-FEB-1998.
 XX
 XX 29-JUL-1997; 97WO-EP04110.
 XX
 XX 30-JUL-1996; 96GB-0015976.
 XX
 PA (CLIN-) CENT CLINICAL & BASIC RES.
 XX
 PI Delaisse J, Foged NT, Meldal M;
 XX
 DR WPI; 1998-130425/12.
 XX
 PT Use of inhibitors of protease(s) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as
 PT osteoporosis
 XX
 PS Example 6b; Page 44; 110pp; English.
 XX
 CC Peptide B is a substrate of matrix metalloproteinase MMP-9. Novel
 CC peptide substrate mimicking MMP-inhibitors (see AAW52132-33) are
 CC promising agents for use in treatment of bone metabolic disease.
 CC They can be used to inhibit proteinases involved in the
 CC recruitment, proliferation, differentiation or migration of
 CC osteoclast precursor cells or in the migration, fusion, attachment,
 CC polarisation, removal of mineralised osseous substance or death of
 CC osteoclasts. The inhibitors reduce the rate of bone resorption
 CC and are used to treat or prevent, e.g. osteoporosis and osteolytic
 CC bone metastases. They are also useful in, e.g. treatment of
 CC cancer, ulcers, arthritis and periodontal disease.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 3
 AAP40807
 ID AAP40807 standard; Protein; 6 AA.
 XX
 AC AAP40807;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Sequence of synthetic peptide substrate for mammalian collagenase.
 XX
 KW Collagenase; proteolytic enzyme; collagen; protein.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Ac-P
 FT Modified-site 6
 FT /label= G-OGH2CH3
 XX
 PN GB2131813-A.
 XX
 PD 27-JUN-1984.
 XX
 XX 15-DEC-1983; 83GB-0033460.
 XX
 PR 16-DEC-1982; 82US-0450318.
 PR 16-MAR-1984; 84US-0590395.
 XX
 XX (MONS) MONSANTO CO.
 PA (MAUS/) MONSANTO CO.
 XX
 PI Weingarten HI;
 XX
 XX WPI; 1984-160555/26.
 XX
 PT Diagnostic hexa:peptide substrate - for determining collagenase
 PT in biological samples
 XX
 PS Claim 3; Page 6; 6pp; English.
 XX
 CC The inventors claim synthetic peptide substrates having high
 CC activity for the enzyme collagenase. The G-L peptide bond (AAs 3-4)
 CC in the peptides of the invention cleaves substantially more readily
 CC with mammalian collagenase than the G-I peptide in the corresponding
 CC posn. of existing peptides. It has also been found that the G-L-L

CC sequence is further rate enhancing in the cleavage reaction with
 CC mammalian collagenase. Thus the peptides of this invention are 2-1/2
 CC times as active as the corresponding peptides contg. the G-I-L
 CC sequence in the same posn.
 XX
 XX SQ Sequence 6 AA;

Query Match 83.3%; Score 25; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgla 5
 |||||
 Db 1 plgla 5

RESULT 4
 AAB01559
 ID AAB01559 standard; peptide: 6 AA.
 AC AAB01559;
 XX

XX 08-NOV-2000 (first entry)
 DT Collagenase substrate site found in collagen.
 DE
 DE Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
 KW sealant; tissue engineering; wound healing; scaffold;
 KW cell transplant; adhesion prevention; cell migration; collagenase;
 KW plasmin; elastase.
 KW
 XX Homo sapiens.
 OS
 XX WO200044808-A1.
 PN
 XX 03-AUG-2000.
 PD
 XX 01-FEB-2000; 2000WO-US02608.
 PF
 XX 01-FEB-1999; 99US-0118093.
 PR
 XX (HUBB/) HUBBELL J A.
 PA

XX Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;
 PI Tirelli N, Vernon B;
 PI
 XX WPI: 2000-524289/47.
 DR
 XX

PT Producing polymeric biomaterials by polymerizing two or more precursor
 PT components (e.g. polymer, protein or peptide) of the biomaterial,
 PT useful for delivering therapeutic molecules to a subject and as
 PT adhesives or sealants
 XX

PS Disclosure; Page 45; 119pp; English.

XX A method of making polymeric biomaterials is described comprising
 CC combining two or more precursor components (e.g. polymer, protein or
 CC peptide) of the biomaterial under conditions that allow
 CC polymerisation of the two components. Polymerisation occurs through
 CC self selective reaction between a strong nucleophile and a conjugated
 CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
 CC addition. The polymeric hydrogels can be used in a variety of
 CC applications. They can be used to deliver therapeutic molecules to
 CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
 CC lung), as tissue engineering and wound healing scaffolds, and as cell
 CC transplant devices. The biomaterials are also useful for adhesion
 CC prevention to minimise unwanted operative or post-traumatic adhesions.
 CC In the instances where the precursor for the polymeric biomaterial
 CC is a peptide, the nucleophile is the amino acid cysteine. This
 CC results in peptides of structure similar to H₂N-CXXXXXXC-XXXXC-COOH
 CC (See GENESQ records AAB01531-B01535). The length of XXXXX is variable
 CC and can be of any number. It is particularly useful when the

CC sequences in the domains shown as XXXXX are substrates for enzymes
 CC that are involved in cell migration (e.g. as substrates for enzymes
 CC such as collagenase, plasmin or elastase).
 XX
 XX SQ Sequence 6 AA;

Query Match 83.3%; Score 25; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgla 5
 |||||
 Db 1 plgla 5

RESULT 5
 AAY31035
 ID AAY31035 standard; peptide: 6 AA.
 XX
 AC AAY31035;
 XX

XX 21-OCT-1999 (first entry)
 DT Non-crosslinked protein particle peptide 84.
 DE
 DE Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 KW
 XX Synthetic.
 OS
 XX US5945033-A.
 PN
 XX 31-AUG-1999.
 PD
 XX 12-NOV-1996; 96US-0747137.
 PF
 XX 14-MAR-1994; 94US-0212546.
 PR
 XX 15-JAN-1991; 91US-0641720.
 PR
 XX 13-OCT-1992; 92US-0859560.
 PR
 XX 01-JUN-1993; 93US-0069831.
 PR
 XX 12-NOV-1996; 96US-0747137.
 PR

XX (HEMO-) HEMOSPHERE INC.
 PA

XX Yen RCK;
 PI
 XX WPI: 1999-508153/42.
 DR
 XX

XX Non-crosslinked protein particles for therapeutic and diagnostic use
 XX
 XX Example 22; Column 83-84; 65pp; English.

XX This invention describes a novel aqueous suspension of monodisperse
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
 CC is stable against dissolving upon dilution with an alcohol-free aqueous
 CC medium. The method involves (a) forming an aqueous solution containing
 CC albumin and hemoglobin and (b) treating the aqueous solution with an
 CC alcohol to cause the solution to become turbid. The particles are useful
 CC as agents for in vivo administration, either of their own administration
 CC or as a vehicle for other therapeutic or diagnostic agents. The method
 CC permits the formation of albumin and hemoglobin particles in the
 CC nanometer and micrometer size range, in a form closer to their natural
 CC form than the forms of the prior art. The particles therefore constitute
 CC a more closely controlled agent for in vivo administration, with greater
 CC ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.
 XX

XX SQ Sequence 6 AA;

Query Match 76.7%; Score 23; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 lglar 6
|||||

Db 2 lglar 6
|||||

RESULT 6

AAB10447
ID AAB10447 standard; peptide; 6 AA.

XX
AC AAB10447;

XX
DT 01-DEC-2000 (first entry)

XX
DE Peptide sequencing method synthetic peptide SEQ ID NO: 3.

XX
KW Peptide sequencing; fragmentation pattern; amino acid modification;
KW post-translational modification; laundry; cleansing product; proteomic;
KW y-ion.

XX
OS Synthetic.

XX
PN WO200043792-A2.

XX
PD 27-JUL-2000.

XX
PF 12-JAN-2000; 2000WO-US00790.

XX
PR 20-JAN-1999; 99US-0116502.

XX
PR 29-SEP-1999; 99US-0156677.

XX
PA (PROC) PROCTER & GAMBLE CO.

XX
PI Keough TW, Youngquist RS;

XX
DR WPI; 2000-543265/49.

XX
PT Determining amino acid sequence of polypeptide by derivatizing the
PT N-terminus of the polypeptide with acidic moieties, analyzing
PT derivatized products using mass spectrometric technique and
PT interpreting the fragmentation pattern -

XX
PS Example 4; Page 29; 30pp; English.

XX
CC This invention describes a novel method for determining the amino acid
CC sequence of a polypeptide comprising derivatizing the N-terminus of the
CC polypeptide or polypeptides with one or more acidic moieties with pK_a of
CC less than 2 when coupled with the polypeptide or polypeptides, analyzing
CC the derivatized products using a mass spectrometric technique to provide
CC a fragmentation pattern free of a- and b-ions and interpreting the
CC fragmentation pattern. The method is used for sequencing wild-type or
CC variant polypeptides. Applications include biological studies,
CC identification of post-translational modifications in proteins,
CC identification of amino acid modifications in variant proteins used in
CC e.g. commercial laundry and cleansing products, designing oligonucleotide
CC probes for gene cloning, rapid characterization of products formed in
CC directed evolution studies, combinatorial chemistry and peptide libraries
CC and proteomics. Derivatization of the polypeptides with acid groups gives
CC almost exclusive y-ion fragmentation and very little a-ion and b-ion
CC 'noise', providing mass spectra which are more easily interpreted. The
CC method is simple, efficient and widely applicable to both wild-type and
CC variant polypeptides. This sequence represents a synthetic peptide used
CC to illustrate the method of the invention.

XX
SQ Sequence 6 AA;

Query Match

Best Local Similarity 76.7%; Score 23; DB 21; Length 6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 lglar 6
|||||

Db 2 lglar 6
|||||

RESULT 7

AAB01557
ID AAB01557 standard; peptide; 6 AA.

XX
AC AAB01557;

XX
DT 08-NOV-2000 (first entry)

XX
DE Collagenase substrate site found in collagen.

XX
KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
KW sealant; tissue engineering; wound healing; scaffold;
KW cell transplant; adhesion prevention; cell migration; collagenase;
KW plasmin; elastase.

XX
OS Homo sapiens.

XX
PN WO200044808-A1.

XX
PD 03-AUG-2000.

XX
PF 01-FEB-2000; 2000WO-US02608.

XX
PR 01-FEB-1999; 99US-0118093.

XX
PA (HUBB/) HUBBELL J A.

XX
PI Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;

XX
PI Tirelli N, Vernon B;

XX
DR WPI; 2000-524289/47.

XX
PT Producing polymeric biomaterials by polymerizing two or more precursor
PT components (e.g. polymer, protein or peptide) of the biomaterial,
PT useful for delivering therapeutic molecules to a subject and as
PT adhesives or sealants

XX
PS Disclosure; Page 45; 119pp; English.

XX
CC A method of making polymeric biomaterials is described comprising
CC combining two or more precursor components (e.g. polymer, protein or
CC peptide) of the biomaterial under conditions that allow
CC polymerisation of the two components. Polymerisation occurs through
CC self selective reaction between a strong nucleophile and a conjugated
CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
CC addition. The polymeric hydrogels can be used in a variety of
CC applications. They can be used to deliver therapeutic molecules to
CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
CC lung), as tissue engineering and wound healing scaffolds, and as cell
CC transplant devices. The biomaterials are also useful for adhesion
CC prevention to minimise unwanted operative or post-traumatic adhesions.
CC In the instances where the precursor for the polymeric biomaterial
CC is a peptide, the nucleophile is the amino acid cysteine. This
CC results in peptides of structure similar to H₂N-CXXXXXXC-COOH
CC (See GENESQ records AAB01531-B01535). The length of XXXX is variable
CC and can be of any number. It is particularly useful when the
CC sequences in the domains shown as XXXXX are substrates for enzymes
CC that are involved in cell migration (e.g. as substrates for enzymes
CC such as collagenase, plasmin or elastase).

XX
SQ Sequence 6 AA;

Query Match

Best Local Similarity 76.7%; Score 23; DB 21; Length 6;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 lglar 5
|||||

Db 1 plgl 5

RESULT 8

AAP30449
ID AAP30449 standard; peptide; 4 AA.XX
AC AAP30449;

DT 04-SEP-1992 (first entry)

XX Substrate for collagenase.

DE Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= X-Pro

FT /note= "X= H or N protecting gp."

FT Modified-site 3

FT /label= Gly(O-Ile)

FT Modified-site 4

FT /label= Leu-X

FT /note= "X= terminal amide, carboxyl or ester gp."

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Substrate for collagenase.

Peptide; peptolide; cleavage.

Synthetic.

Key

Modified-site 1

/label= X-Pro

/note= "X= H or N protecting gp."

Modified-site 3

/label= Gly(O-Leu)

Modified-site 4

/label= Leu-X

/note= "X= terminal amide, carboxyl or ester gp."

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Substrate for collagenase.

Peptide; peptolide; cleavage.

Synthetic.

Key

Modified-site 1

/label= X-Pro

/note= "X= H or N protecting gp."

Modified-site 3

/label= Gly(O-Leu)

Modified-site 4

/label= Leu-X

/note= "X= terminal amide, carboxyl or ester gp."

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Substrate for collagenase.

Peptide; peptolide; cleavage.

Synthetic.

Key

Modified-site 1

/label= X-Pro

/note= "X= H or N protecting gp."

Modified-site 3

/label= Gly(O-Ile)

Modified-site 4

/label= Leu-X

/note= "X= terminal amide, carboxyl or ester gp."

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Substrate for collagenase.

Peptide; peptolide; cleavage.

Synthetic.

Key

Modified-site 1

/label= X-Pro

/note= "X= H or N protecting gp."

Modified-site 3

/label= Gly(O-Ile)

Modified-site 4

/label= Leu-X

/note= "X= terminal amide, carboxyl or ester gp."

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PD 23-APR-1998.
XX
XX PF 15-OCT-1997; 97WO-US18538.
XX
XX PF 15-OCT-1996; 96US-0027544.
XX
XX (LIPO ) LIPOSOME CO INC.
XX
XX Ali S, Cabral-Lilly D, Erukulla RK, Franklin JC;
PI Janoff AS, Meers PR, Pak C;
XX
XX WPI; 1998-261025/23.
XX
XX New peptide-lipid conjugates are incorporated into liposome(s) - to
PT selectively destabilise the liposome(s) in the vicinity of target
PT peptidase-secreting cells, e.g., tumour cells; useful in diagnosis
PT and therapy
XX
XX Claim 8; Page 33; 55pp; English.
XX
XX The invention relates to peptide-lipid conjugates and their use in
CC the preparation of liposomes which are predisposed to degradation in the
CC presence of peptidase-secreting cells and hence are targeted to these
CC cells. The liposomes can be used to treat mammalian diseases, disorders
CC and conditions, e.g. tumours, microbial infections and inflammation. The
CC liposomes allow selective delivery of an active agent to desired cells.
CC The liposomes are stable when the peptide remains conjugated to the
CC lipid. However, once the peptide portion of the conjugate is cleaved
CC from the lipid, by the action of cell-secreted peptidases, the liposomes
CC destabilise and release their contents in the vicinity of, or into, the
CC secreting cells. The liposomes can thus be used to treat conditions
CC characterised by the occurrence of peptidase-secreting cells. For
CC example, the breast cancer cell line MCF-7 is known to secrete elastase,
CC the levels of which are inversely correlated to overall survival in
CC breast cancer patients. The present sequence represents a specifically
CC claimed peptide which forms part of the peptide-lipid conjugate.
XX
XX Sequence 4 AA;
SQ

Query Match 70.0%; Score 21; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plql 4
Db 1 plql 4

RESULT 11
AAB62798
ID AAB62798 standard; peptide; 4 AA.
XX
XX AAB62798;
XX
XX 03-APR-2001 (first entry)
XX
XX Peptide-lipid conjugate peptide #13.
XX
XX Peptide-lipid conjugate; liposome; liposomal drug delivery; cancer;
KW peptidase-secreting cell; phosphatidylethanolamine;
KW inflammatory disorder; neuropathy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= OTHER
FT /note= "optionally modified by methoxysuccinyl or
FT succinyl group"
FT Modified-site 4
FT /label= OTHER
FT /note= "C-terminal phosphatidylethanolamine"
XX

PD 23-APR-1998.
XX
XX PF 15-OCT-1997; 97WO-US18538.
XX
XX PF 15-OCT-1996; 96US-0027544.
XX
XX (LIPO ) LIPOSOME CO INC.
XX
XX Ali S, Cabral-Lilly D, Erukulla RK, Franklin JC;
PI Janoff AS, Meers PR, Pak C;
XX
XX WPI; 1998-261025/23.
XX
XX New peptide-lipid conjugates are incorporated into liposome(s) - to
PT selectively destabilise the liposome(s) in the vicinity of target
PT peptidase-secreting cells, e.g., tumour cells; useful in diagnosis
PT and therapy
XX
XX Claim 8; Page 33; 55pp; English.
XX
XX The invention relates to peptide-lipid conjugates and their use in
CC the preparation of liposomes which are predisposed to degradation in the
CC presence of peptidase-secreting cells and hence are targeted to these
CC cells. The liposomes can be used to treat mammalian diseases, disorders
CC and conditions, e.g. tumours, microbial infections and inflammation. The
CC liposomes allow selective delivery of an active agent to desired cells.
CC The liposomes are stable when the peptide remains conjugated to the
CC lipid. However, once the peptide portion of the conjugate is cleaved
CC from the lipid, by the action of cell-secreted peptidases, the liposomes
CC destabilise and release their contents in the vicinity of, or into, the
CC secreting cells. The liposomes can thus be used to treat conditions
CC characterised by the occurrence of peptidase-secreting cells. For
CC example, the breast cancer cell line MCF-7 is known to secrete elastase,
CC the levels of which are inversely correlated to overall survival in
CC breast cancer patients. The present sequence represents a specifically
CC claimed peptide which forms part of the peptide-lipid conjugate.
XX
XX Sequence 4 AA;
SQ

Query Match 70.0%; Score 21; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plql 4
Db 1 plql 4

RESULT 12
AAP40806
ID AAP40806 standard; peptide; 6 AA.
XX
XX AAP40806;
XX
XX 29-JUL-1992 (first entry)
XX
XX Sequence of synthetic peptide substrate for mammalian collagenase.
XX
XX Collagenase; proteolytic enzyme; collagen; protein.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /label= Ac-P
FT Modified-site 6
FT /label= G-OCH2CH3
XX
XX GB2131813-A.
XX
XX 27-JUN-1984.
XX
XX 15-DEC-1983; 83GB-0033460.
XX
XX 16-DEC-1982; 82US-0450318.
XX
XX 16-MAR-1984; 84US-0590395.
XX
XX (MONS ) MONSANTO CO.
PA (MAUS/) MONSANTO CO.
XX
XX Weingarten HI;
XX

```


DR WPI; 1984-160555/26.
 XX Diagnostic hexa-peptide substrate - for determining collagenase
 PT in biological samples
 PS Claim 2; Page 6; 6pp; English.
 XX The inventors claim synthetic peptide substrates having high
 CC activity for the enzyme collagenase. The G-L peptide bond (AAs 3-4)
 CC in the peptides of the invention cleaves substantially more readily
 CC with mammalian collagenase than the G-I peptide in the corresponding
 CC posn. of existing peptides. It has also been found that the G-L-L
 CC sequence is further rate enhancing in the cleavage reaction with
 CC mammalian collagenase. Thus the peptides of this invention are 2-1/2
 CC times as active as the corresponding peptides contg. the G-I-L
 CC sequence in the same posn.
 XX Sequence 6 AA;
 SQ

Query Match 70.0%; Score 21; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

RESULT 13
 AAW24981
 ID AAW24981 standard; peptide: 6 AA.
 AC AAW24981;
 XX
 XX
 DT 03-DEC-1997 (first entry)
 DE Recombinant human gelatinase thiopeptolide substrate.
 XX
 XX Catalytic domain; human; gelatinase; matrix metalloprotease; propeptide;
 KW hemopexin; fibronectin; vector; recombinant; deletion; hernia; joint;
 KW vertebral disc; dermal ulcer; scar tissue.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acetylated N-terminus"
 FT
 FT Misc-difference 3..4
 FT /note= "amino acid residues linked by thioester bond"
 FT Modified-site 6
 FT /note= "Gly-OEt"
 XX
 PN US5646027-A.
 XX
 XX 08-JUL-1997.
 PD
 XX
 XX 08-SEP-1994; 94US-0303270.
 PF
 XX 08-SEP-1994; 94US-0303270.
 XX
 PR (WARN) WARNER LAMBERT CO.
 XX
 XX Hupe DJ, Johnson LL, Ye Q;
 PI
 XX WPI; 1997-362935/33.
 DR
 XX Production of recombinant human gelatinase catalytic domain protein
 PT - especially using vector containing new synthetic coding sequence
 XX
 XX Example 3; Column 10; 2lpp; English.
 PS
 XX This peptide is a substrate for a novel recombinant catalytic domain of

CC the human 72 kD gelatinase, a member of the matrix metalloprotease
 CC family, lacking its propeptide, C-terminal hemopexin-like domain or
 CC fibronectin-like insert (AAW24980). The catalytic domain protein is
 CC useful for treating herniated vertebral discs, treating dermal ulcers,
 CC modifying scar tissue formation and treating joint diseases.
 XX
 SQ Sequence 6 AA;
 CC

Query Match 70.0%; Score 21; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

RESULT 14
 AAB37325
 ID AAB37325 standard; Peptide: 6 AA.
 XX
 AC AAB37325;
 XX
 DT 19-FEB-2001 (first entry)
 DE Peptide linker #10.
 XX
 XX Cytostatic; antiproliferative; vascular endothelial growth factor;
 KW VEGF; antibody; VEGF2 receptor; cancer; vascularised solid tumour;
 KW peptide linker.
 XX
 OS Unidentified.
 XX
 PN WO200064946-A2.
 XX
 XX 02-NOV-2000.
 PD
 XX 28-APR-2000; 2000WO-US11367.
 PF
 XX 28-APR-1999; 99US-0131432.
 PR (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Thorpe PE, Brekken RA;
 PI
 XX WPI; 2000-687317/67.
 DR
 XX Immunogenic composition for the treatment and diagnosis of cancer
 PT comprises an anti-VEGF (vascular endothelial growth factor) antibody
 PT binding the same epitope as the monoclonal antibody ATCC PTA 1595 -
 XX
 XX Disclosure; Page 150; 298pp; English.
 PS
 XX The present invention relates to anti-Vascular Endothelial Growth Factor
 CC (VEGF) antibodies that bind to the same epitope as the monoclonal
 CC antibody ATCC PTA 1595 and which significantly inhibit VEGF binding to
 CC the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF
 CC receptor VEGFR1. The present sequence is a peptide linker which can be
 CC used to link the antibodies of the present invention to anti-cellular or
 CC cytotoxic agents. The anti-VEGF antibodies of the present invention are
 CC useful for the treatment and diagnosis of cancer, especially vascularised
 CC solid tumours.
 XX
 SQ Sequence 6 AA;
 CC

Query Match 70.0%; Score 21; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

Db 1 plgl 4

RESULT 15

AAB15681
ID AAB15681 standard; peptide; 6 AA.

XX AC AAB15681;

XX DT 08-JAN-2001 (first entry)

XX DE Matrix metalloprotease-sensitive linker peptide.

XX KW Matrix metalloprotease; MMP; restriction protease;

XX KW protease-sensitive linker; stabilon; stabilising fusion peptide;

XX KW single-chain antibody; vaccine; gene therapy;

XX KW protein degradation modulation; protein stability; Alzheimer's disease.

XX OS Unidentified.

XX PN WO200042185-A1.

XX PD 20-JUL-2000.

XX PF 11-JAN-2000; 2000WO-US00558.

XX PR 11-JAN-1999; 99US-0115505.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX PI (MCIN/) MCINNIS P A.

XX PI Chain DG;

XX DR WPI; 2000-476059/41.

XX PT Modulating degradability of protein or peptide useful for gene therapy

XX PT involving antibodies, comprises altering a gene at the N terminus to

XX PT render protein or peptide metabolically stable -

XX PS Disclosure; Page 12; 76pp; English.

XX CC The present sequence is a peptide which is sensitive to matrix

XX CC metalloprotease (MMP). It may be used to link a stabilising fusion

XX CC peptide, referred to as a stabilon, to the N-terminus of a single-chain

XX CC antibody. The stabilon increases stability of the antibody against

XX CC proteolysis in vivo. Induction of expression of MMP by means of an

XX CC inducible promoter causes cleavage of the linker and removal of the

XX CC stabilon. This renders the antibody susceptible to proteolysis by the

XX CC N-end rule pathway. Attachment of the stabilon to the antibody through a

XX CC protease-sensitive linker region therefore allows modulation of antibody

XX CC stability. Stabilised recombinant proteins may be used in gene therapy

XX CC for the treatment of disorders such as Alzheimer's disease.

XX SQ Sequence 6 AA;

Query Match 70.0%; Score 21; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4

Db 1 plgl 4

Search completed: February 28, 2002, 16:51:00

Job time: 195 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:50:15 ; Search time 90.37 seconds
(without alignments)
18.435 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 89186

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	18 US-09-464-908-1	Sequence 1, Appli
2	25	83.3	6	18 US-09-496-231A-31	Sequence 31, Appl
3	25	83.3	6	22 US-09-808-832-75	Sequence 75, Appl
4	23	76.7	6	18 US-09-496-231A-29	Sequence 29, Appl
5	21	70.0	4	15 US-09-101-167-23	Sequence 15, Appl
6	21	70.0	4	15 US-09-168-010-15	Sequence 15, Appl
7	21	70.0	4	15 US-09-168-010-20	Sequence 20, Appl
8	21	70.0	4	15 US-09-168-010-21	Sequence 21, Appl
9	21	70.0	4	17 US-09-343-650-15	Sequence 15, Appl

10	21	70.0	4	17 US-09-343-650-20	Sequence 20, Appl
11	21	70.0	4	17 US-09-343-650-21	Sequence 21, Appl
12	21	70.0	4	21 US-09-704-251-13	Sequence 13, Appl
13	21	70.0	4	22 US-09-808-832-203	Sequence 203, App
14	21	70.0	4	23 US-09-772-772-13	Sequence 13, Appl
15	21	70.0	5	22 US-09-808-832-8	Sequence 8, Appl
16	21	70.0	5	22 US-09-808-832-16	Sequence 16, Appl
17	21	70.0	5	22 US-09-808-832-205	Sequence 205, App
18	21	70.0	5	22 US-09-808-832-206	Sequence 206, App
19	21	70.0	6	13 US-08-909-601-34	Sequence 34, Appl
20	21	70.0	6	13 US-08-909-601-34	Sequence 34, Appl
21	21	70.0	6	13 US-08-909-607-34	Sequence 34, Appl
22	21	70.0	6	18 US-09-496-231A-30	Sequence 30, Appl
23	21	70.0	6	19 US-09-561-005-24	Sequence 24, Appl
24	21	70.0	6	19 US-09-561-108-24	Sequence 24, Appl
25	21	70.0	6	19 US-09-561-499-24	Sequence 24, Appl
26	21	70.0	6	19 US-09-561-500-24	Sequence 24, Appl
27	21	70.0	6	19 US-09-561-526-24	Sequence 24, Appl
28	21	70.0	6	19 US-09-562-245-24	Sequence 24, Appl
29	21	70.0	6	20 US-09-639-667-7	Sequence 7, Appl
30	21	70.0	6	20 US-09-640-198-9	Sequence 9, Appl
31	21	70.0	6	20 US-09-640-198-11	Sequence 11, Appl
32	21	70.0	6	21 US-09-753-078-3	Sequence 3, Appl
33	21	70.0	6	22 US-09-808-832-39	Sequence 39, Appl
34	21	70.0	6	22 US-09-808-832-52	Sequence 52, Appl
35	21	70.0	6	22 US-09-808-832-53	Sequence 53, Appl
36	21	70.0	6	22 US-09-808-832-54	Sequence 54, Appl
37	21	70.0	6	22 US-09-808-832-58	Sequence 58, Appl
38	21	70.0	6	22 US-09-808-832-59	Sequence 59, Appl
39	21	70.0	6	22 US-09-808-832-60	Sequence 60, Appl
40	21	70.0	6	22 US-09-808-832-61	Sequence 61, Appl
41	21	70.0	6	22 US-09-808-832-62	Sequence 62, Appl
42	21	70.0	6	22 US-09-808-832-65	Sequence 65, Appl
43	21	70.0	6	22 US-09-808-832-71	Sequence 71, Appl
44	21	70.0	6	22 US-09-808-832-73	Sequence 73, Appl
45	21	70.0	6	22 US-09-808-832-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-464-908-1
; Sequence 1, Application US/09464908
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; TITLE OF INVENTION: Selective Inhibitors Of MMP-12
; FILE REFERENCE: HMR2026A
; CURRENT APPLICATION NUMBER: US/09/464,908
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/155,223
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-464-908-1

Query Match 100.0%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 1 PLGLAR 6

RESULT 2

US-09-496-231A-31

; Sequence 31, Application US/09496231A

GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Elbert, Donald
; APPLICANT: Lutolf, Matthias
; APPLICANT: Pratt, Allison
; APPLICANT: Schoenmakers, Ronald
; APPLICANT: Tirelli, Nicola
; APPLICANT: Vernon, Brent
; TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC
; TITLE OF INVENTION: ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS
; FILE REFERENCE: 50154/002002
; CURRENT APPLICATION NUMBER: US/09/496,231A
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-496-231A-31

Query Match 83.3%; Score 25; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | |
Db 1 PLGLA 5

RESULT 3

US-09-808-832-75
; Sequence 75, Application US/09808832
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Phosphatidylcholine, targeted antineoplastic drugs and their ther
; TITLE OF INVENTION: use
; FILE REFERENCE: PH-7134
; CURRENT APPLICATION NUMBER: US/09/808,832
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,387
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: acetyl-glycine
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A pep
; OTHER INFORMATION: tide synthesizer using readily available materials well known to
; OTHER INFORMATION: ordinarily skilled artisans
US-09-808-832-75

Query Match 83.3%; Score 25; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | |
Db 2 PLGLA 6

RESULT 4

US-09-496-231A-29
; Sequence 29, Application US/09496231A
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Elbert, Donald
; APPLICANT: Lutolf, Matthias
; APPLICANT: Pratt, Allison
; APPLICANT: Schoenmakers, Ronald
; APPLICANT: Tirelli, Nicola
; APPLICANT: Vernon, Brent
; TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC
; TITLE OF INVENTION: ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS
; FILE REFERENCE: 50154/002002
; CURRENT APPLICATION NUMBER: US/09/496,231A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/118,093
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-496-231A-29

Query Match 76.7%; Score 23; DB 18; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | |
Db 1 PLGLA 5

RESULT 5

US-09-101-167-23
; Sequence 23, Application US/09101167A
; GENERAL INFORMATION:
; APPLICANT: TE KOPPEL, Johannes M
; APPLICANT: BECKMAN, Bob
; TITLE OF INVENTION: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING
; TITLE OF INVENTION: FLUORESCENCE-QUENCHED SUBSTRATES
; FILE REFERENCE: TE KOPPEL et al. 09/101,167
; CURRENT APPLICATION NUMBER: US/09/101,167A
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: EP 96200017.0
; EARLIER FILING DATE: 1996-01-04
; EARLIER APPLICATION NUMBER: PCT/NL97/00002
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:UNKNOWN
US-09-101-167-23

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 6

US-09-168-010-15
; Sequence 15, Application US/09168010

GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
US-09-168-010-15

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 7
US-09-168-010-20
Sequence 20, Application US/09168010
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-168-010-20

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 8
US-09-168-010-21
Sequence 21, Application US/09168010
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal succinyl group
US-09-168-010-21

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 9
US-09-343-650-15
Sequence 15, Application US/09343650
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Meers, Paul
APPLICANT: Pak, Charles
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
TITLE OF INVENTION: Liposomal Drug Delivery
FILE REFERENCE: TLC 215c
CURRENT APPLICATION NUMBER: US/09/343,650
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 08/950,618
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
US-09-343-650-15

Query Match 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 10

US-09-343-650-20
; Sequence 20, Application US/09343650
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Meers, Paul
; APPLICANT: Pak, Charles
; APPLICANT: Ali, Shaikat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
; FILE REFERENCE: TLC 215c
; CURRENT APPLICATION NUMBER: US/09/343,650
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 08/950,618
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-343-650-20

Query Match

Best Local Similarity 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 11

US-09-343-650-21
; Sequence 21, Application US/09343650
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Meers, Paul
; APPLICANT: Pak, Charles
; APPLICANT: Ali, Shaikat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
; FILE REFERENCE: TLC 215c
; CURRENT APPLICATION NUMBER: US/09/343,650
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 08/950,618
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides

; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
US-09-343-650-21

Query Match 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 12

US-09-704-251-13
; Sequence 13, Application US/09704251
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lilly
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-09-704-251-13

Query Match

Best Local Similarity 70.0%; Score 21; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 13

US-09-808-832-203
; Sequence 203, Application US/09808832
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their t
; FILE REFERENCE: PH-7134
; CURRENT APPLICATION NUMBER: US/09/808,832
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,387
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 203
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(4)
; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A
; OTHER INFORMATION: tide synthesizer using readily available materials well known
; OTHER INFORMATION: ordinarily skilled artisans

US-09-808-832-203

Query Match 70.0%; Score 21; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 | | | |
Db 1 PLGL 4

RESULT 14

US-09-972-772-13
; Sequence 13, Application US/09972772
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; FILE REFERENCE: PPI-106CP
; CURRENT APPLICATION NUMBER: US/09/972,772
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-09-972-772-13

Query Match 70.0%; Score 21; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 | | | |
Db 1 PLGL 4

RESULT 15

US-09-808-832-8
; Sequence 8, Application US/09808832
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their ther
; TITLE OF INVENTION: use
; FILE REFERENCE: PH-7134
; CURRENT APPLICATION NUMBER: US/09/808,832
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,387
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A pep
; OTHER INFORMATION: tide synthesizer using readily available materials well known to
; OTHER INFORMATION: ordinarily skilled artisans
US-09-808-832-8

Query Match 70.0%; Score 21; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 | | | |
Db 1 PLGL 4

Search completed: February 28, 2002, 16:53:15
Job time: 180 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:50:35 ; Search time 14.07 Seconds
(without alignments)
24.143 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 258822 seqs, 56616433 residues

Total number of hits satisfying chosen parameters: 12908

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgn2.6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2.6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2.6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2.6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2.6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2.6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2.6/ptodata/2/paa/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	70.0	4	6	US-10-001-945-13
2	21	70.0	5	5	US-09-560-390-32
3	21	70.0	6	5	US-09-560-390-22
4	21	70.0	6	5	US-09-560-390-25
5	21	70.0	6	5	US-09-560-390-24
6	17	56.7	4	5	US-09-998-831-24
7	17	56.7	4	5	US-09-451-206-17
8	17	56.7	4	5	US-09-914-541-22
9	17	56.7	4	6	US-10-001-945-1
10	17	56.7	4	6	US-10-001-945-14
11	17	56.7	5	1	PCT-US01-27692A-71
12	17	56.7	5	1	PCT-US01-27702A-256
13	17	56.7	5	5	US-09-560-390-2
14	17	56.7	5	5	US-09-560-390-18
15	17	56.7	5	5	US-09-560-390-21
16	17	56.7	5	5	US-09-560-390-24
17	17	56.7	5	5	US-09-104-337A-321
18	17	56.7	6	5	US-09-560-390-5
19	17	56.7	6	5	US-09-155-613A-91
20	16	53.3	5	6	US-10-001-945-33
21	15	50.0	5	1	PCT-US01-28044A-364
22	15	50.0	5	5	US-09-560-390-19
23	15	50.0	6	1	PCT-US01-27702A-268
24	15	50.0	6	5	US-09-604-145-5
25	15	50.0	6	6	US-10-001-945-19
26	14	46.7	3	1	PCT-US01-28044A-363

Sequence 62, Appl
Sequence 8933, Ap
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 1203, App
Sequence 587, App
Sequence 9145, Ap
Sequence 15, Appl
Sequence 21, Appl
Sequence 2895, Ap
Sequence 616, App
Sequence 775, App
Sequence 616, App
Sequence 616, App
Sequence 587, App
Sequence 62, Appl
Sequence 4, Appl
Sequence 62, Appl
Sequence 8933, Ap
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 1203, App
Sequence 587, App
Sequence 9145, Ap
Sequence 15, Appl
Sequence 21, Appl
Sequence 2895, Ap
Sequence 616, App
Sequence 775, App
Sequence 616, App
Sequence 616, App
Sequence 587, App
Sequence 62, Appl
Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-001-945-13

; Sequence 13, Application US/10001945

; GENERAL INFORMATION:

; APPLICANT: Olson, Gary L.

; APPLICANT: Self, Christopher

; APPLICANT: Lee, Lily

; APPLICANT: Cook, Charles M.

; APPLICANT: Birktoft, Jens

; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE

; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS

; FILE REFERENCE: PPI-106CP2

; CURRENT APPLICATION NUMBER: US/10/001,945

; CURRENT FILING DATE: 2001-11-01

; PRIOR APPLICATION NUMBER: US 09/972,772

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: US 09/704,251

; PRIOR FILING DATE: 2000-11-01

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Motifs

US-10-001-945-13

Query Match

Best Local Similarity 70.0%; Score 21; DB 6; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4

Db 1 PLGL 4

RESULT 2

US-09-560-390-32

; Sequence 32, Application US/09560390

; GENERAL INFORMATION:

; APPLICANT: Pachence Ph.D., James M.

; APPLICANT: Belinka, Benjamin A.

; APPLICANT: Ramani, Thulasi

; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES

; FILE REFERENCE: 114914.102

; CURRENT APPLICATION NUMBER: US/09/560,390

; CURRENT FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-32

Query Match 70.0%; Score 21; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
||||
Db 1 PLGL 4

RESULT 3
US-09-560-390-22
; Sequence 22, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-22

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
||||
Db 1 PLGL 4

RESULT 4
US-09-560-390-25
; Sequence 25, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-25

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
||||

Db 1 PLGL 4

RESULT 5
US-09-998-831-24
; Sequence 24, Application US/09998831
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; TITLE OF INVENTION: INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998.831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-998-831-24

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
||||
Db 1 PLGL 4

RESULT 6
US-09-451-206-17
; Sequence 17, Application US/09451206
; GENERAL INFORMATION:
; APPLICANT: STEDRONSKY, Erwin R.
; APPLICANT: CAPPELLO, Joseph
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; CROSSLINKING
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: Four Embarcadero Center, Suite 200
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,206
; FILING DATE: 29-Nov-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,246
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertlam I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A61127-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-451-206-17

Query Match 56.7%; Score 17; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
DB 1 PLG 3

RESULT 7

US-09-914-541-22
Sequence 22, Application US/09914541
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF TENNESSEE RESEARCH CORPORATION
APPLICANT: BECKER, JEFFREY M.
APPLICANT: HAUSER, MELINDA
APPLICANT: DONHARDT, AMY
APPLICANT: BARNES, DAVID
TITLE OF INVENTION: EUKARYOTIC PEPTIDE UPTAKE SYSTEM FOR TRANSPORTING
TITLE OF INVENTION: ENKEPHALINS
FILE REFERENCE: 1046-PCT-00
CURRENT APPLICATION NUMBER: US/09/914,541
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: PCT/US00/05158
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,312
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 22
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Tyr-Mif-1
US-09-914-541-22

Query Match 56.7%; Score 17; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
DB 2 PLG 4

RESULT 8

US-10-001-945-1
Sequence 1, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
FILE REFERENCE: PPI-106CP2
CURRENT APPLICATION NUMBER: US/10/001,945
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 09/972,772
PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 09/704,251
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: Xaa at position 4 may be any amino acid
OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-1

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
DB 1 PLG 3

RESULT 9

US-10-001-945-14
Sequence 14, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
FILE REFERENCE: PPI-106CP2
CURRENT APPLICATION NUMBER: US/10/001,945
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 09/972,772
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 09/704,251
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-14

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
DB 1 PLG 3

RESULT 10

US-10-001-945-27
Sequence 27, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE

; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP2
; CURRENT APPLICATION NUMBER: US/10/001.945
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 09/972.772
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704.251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-27

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4

RESULT 11
PCT-US01-27692A-71
; Sequence 71, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(5)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-71

Query Match 56.7%; Score 17; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 3 PLG 5

RESULT 12
PCT-US01-27702A-256
; Sequence 256, Application PC/TUS0127702A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27702A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 256
; LENGTH: 5
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(5)
; OTHER INFORMATION: synthetic construct
PCT-US01-27702A-256

Query Match 56.7%; Score 17; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 3 PLG 5

RESULT 13
US-09-560-390-2
; Sequence 2, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-2

Query Match 56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4

RESULT 14
US-09-560-390-18
; Sequence 18, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-18

Query Match 56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4

```

RESULT 15
US-09-560-390-21
; Sequence 21, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-21

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Query Match      56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
   |||
Db 1 PLG 3

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Search completed: February 28, 2002, 16:55:13
Job time: 278 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 28, 2002, 16:49:25 ; Search time 12.46 seconds
(without alignments)
10.836 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 piglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 21252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 27062

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	76.7	6	2	US-08-747-137-84
2	21	70.0	4	3	US-08-950-618-15
3	21	70.0	4	3	US-08-950-618-20
4	21	70.0	4	3	US-08-950-618-21
5	21	70.0	4	3	US-09-101-167-23
6	21	70.0	4	4	US-09-168-010-15
7	21	70.0	4	4	US-09-168-010-20
8	21	70.0	4	4	US-09-168-010-21
9	21	70.0	6	1	US-08-303-270-8
10	21	70.0	6	4	US-09-208-684-12
11	21	70.0	6	4	US-08-281-313-8
12	19	63.3	6	2	US-08-520-455A-7
13	19	63.3	5	3	US-09-008-308-50
14	18	60.0	6	4	US-08-793-701-9
15	18	60.0	6	1	US-08-014-979-97
16	18	60.0	6	1	US-08-213-897A-17
17	18	60.0	6	2	US-08-188-583-47
18	18	60.0	6	3	US-08-997-918-54
19	18	60.0	6	3	US-09-008-308-60
20	17	56.7	4	1	US-08-219-156-5
21	17	56.7	4	1	US-08-238-089-5
22	17	56.7	4	1	US-08-238-089-6
23	17	56.7	4	1	US-08-366-783-8
24	17	56.7	4	1	US-08-432-651A-5
25	17	56.7	4	1	US-08-432-651A-6
26	17	56.7	4	2	US-08-707-237A-97
27	17	56.7	4	2	US-08-846-021A-11

28	17	56.7	4	3	US-08-642-246-17	Sequence 17, Appl
29	17	56.7	4	3	US-08-962-962C-5	Sequence 5, Appl
30	17	56.7	4	3	US-08-962-962C-6	Sequence 6, Appl
31	17	56.7	4	5	PCT-US95-05560-5	Sequence 5, Appl
32	17	56.7	4	5	PCT-US95-05560-6	Sequence 6, Appl
33	17	56.7	4	5	PCT-US96-06229-17	Sequence 17, Appl
34	17	56.7	5	1	US-08-221-582A-4	Sequence 4, Appl
35	17	56.7	5	1	US-08-219-156-2	Sequence 2, Appl
36	17	56.7	5	1	US-08-219-156-4	Sequence 4, Appl
37	17	56.7	5	1	US-08-219-156-6	Sequence 6, Appl
38	17	56.7	5	1	US-08-219-156-7	Sequence 7, Appl
39	17	56.7	5	1	US-08-219-156-8	Sequence 8, Appl
40	17	56.7	5	1	US-08-238-089-31	Sequence 31, Appl
41	17	56.7	5	1	US-08-238-089-32	Sequence 32, Appl
42	17	56.7	5	1	US-08-213-897A-4	Sequence 4, Appl
43	17	56.7	5	1	US-08-213-897A-15	Sequence 15, Appl
44	17	56.7	5	1	US-08-432-651A-31	Sequence 31, Appl
45	17	56.7	5	1	US-08-432-651A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-747-137-84
; Sequence 84, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-84

Query Match 76.7%; Score 23; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 lglar 6
| | | | |
Db 2 LGLAR 6

RESULT 2
US-08-950-618-15
; Sequence 15, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
US-08-950-618-15

Query Match 70.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 3
US-08-950-618-20
; Sequence 20, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides

; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
US-08-950-618-20

Query Match 70.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 4
US-08-950-618-21
; Sequence 21, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
US-08-950-618-21

Query Match 70.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 5
US-08-950-618-23
; Sequence 23, Application US/09101167B
; Patent No. 6127139
; GENERAL INFORMATION:
; APPLICANT: TE KOPPELE, Johannes M
; APPLICANT: BECKMAN, Bob
; TITLE OF INVENTION: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING
; FILE REFERENCE: FLUORESCENCE-QUENCHED SUBSTRATES
; FILE REFERENCE: TE KOPPELE et al. 09/101,167
; CURRENT APPLICATION NUMBER: US/09/101,167B
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: EP 96200017.0
; EARLIER FILING DATE: 1996-01-04
; EARLIER APPLICATION NUMBER: PCT/NL97/00002
; EARLIER FILING DATE: 1997-01-02

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
US-09-101-167-23

Query Match 70.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 6
US-09-168-010-15
; Sequence 15, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
US-09-168-010-15

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 7
US-09-168-010-20
; Sequence 20, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same

; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-168-010-20

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 8
US-09-168-010-21
; Sequence 21, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; TITLE OF INVENTION: Delivery Using Same
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
US-09-168-010-21

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 9
US-08-303-270-8
; Sequence 8, Application US/08303270
; Patent No. 5646027

```

; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Gelatinase Catalytic Domain Protein
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,270
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 5120-FJT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Thiolester-bond
; LOCATION: 3..4
;
US-08-303-270-8

```

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Query Match 70.0%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 10
US-09-208-684-12
; Sequence 12, Application US/09208684
; Patent No. 6224903
; GENERAL INFORMATION:
; APPLICANT: Francis J. Martin
; APPLICANT: Samuel Zalipsky
; TITLE OF INVENTION: Polymer-Lipid Conjugate for Fusion of
; FILE REFERENCE: 5325-0148.32
; CURRENT APPLICATION NUMBER: US/09/208,684
; EARLIER FILING DATE: 1998-12-10
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: 60/028,269
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT

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; ORGANISM: Homo Sapiens
US-09-208-684-12

Query Match 70.0%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 11
US-08-281-313-8
; Sequence 8, Application US/08281313
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Baragi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,313
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,705
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 4415-01-FJT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Thiolester-bond
; LOCATION: 3..4
;
US-08-281-313-8

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Query Match 70.0%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

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RESULT 12
US-08-520-455A-7
; Sequence 7, Application US/08520455A
; Patent No. 5872207
; GENERAL INFORMATION:
; APPLICANT: Morgan, Barry Arnold
; APPLICANT: Ator, Mark Alan
; APPLICANT: Gainor, James Arthur
; APPLICANT: Gordon, Thomas Douglas
; APPLICANT: Kruse, Lawrence Ivan
; APPLICANT: Sishaan, Teruna Jaya
; TITLE OF INVENTION: N-terminal Marked Peptides Immobilized
; TITLE OF INVENTION: on Glass beads and Method of Preparation and Method of Use The
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sanofi Pharmaceuticals, Inc.
; STREET: 9 Great Valley Parkway, P.O. Box 3026
; CITY: Malvern
; STATE: PA
; COUNTRY: USA
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: Dell Optiplex Gxi
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Microsoft Word 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,455A
; FILING DATE: August 29, 1995
; CLASSIFICATION: 530
; APPLICATION NUMBER: US/08/520,455A
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William J. Davis
; REGISTRATION NUMBER: 30,744
; REFERENCE/DOCKET NUMBER: 61887-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 889-8802
; TELEFAX: (610) 889-8799
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-520-455A-7

Query Match 63.3%; Score 19; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plgla 5
Db 2 PLALA 6

RESULT 13
US-09-008-308-50
; Sequence 50, Application US/09008308
; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heidtmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,308
FILING DATE: 16-JAN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197 01 141.1
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-008-308-50

Query Match 63.3%; Score 19; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plgla 5
Db 2 PQGLA 6

RESULT 14
US-08-793-701-9
; Sequence 9, Application US/08793701
; Patent No. 6248581
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, Brigitte
; APPLICANT: LIM, Eng Mong
; APPLICANT: PORTNOI, Denis
; APPLICANT: BERTHET, Francois-Xavier
; APPLICANT: TIMM, Juliano
; TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR
; TITLE OF INVENTION: EXPRESSION VECTORS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &
; ADDRESSEE: DUNNER, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,701
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR9501133
;; FILING DATE: 30-AUG-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 94/10585
;; FILING DATE: 02-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, Leslie A.
;; REGISTRATION NUMBER: 34,872
;; REFERENCE/DOCKET NUMBER: 02356.0075
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4132
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-793-701-9

Query Match 60.0%; Score 18; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PVGL 4

RESULT 15
US-08-014-979-97
; Sequence 97, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-014-979-97

Query Match 60.0%; Score 18; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plgla 5
Db 2 PYGMA 6

Search completed: February 28, 2002, 16:51:19
Job time: 114 sec

